



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 160341

TO: Minh-Tam Davis  
Location: REM-3A24&3C18  
Art Unit: 1642  
Thursday, July 28, 2005  
Case Serial Number: 09/967305

From: Barb O'Bryen  
Location: Biotech-Chem Library  
Remsen 1a69  
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

### Search Notes

# RUSH

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 10:42:00 ; Search time 841 Seconds  
(without alignments)  
8811.362 Million cell updates/sec

Title: US-09-967-305-3

Perfect score: 1146

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 7277826 seqs, 3233139505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2          | 1146  | 100.0       | 2005      | 9  | US-09-967-305-1   |
| 3          | 1146  | 100.0       | 2005      | 9  | US-09-967-305-10  |
| 4          | 1146  | 100.0       | 2005      | 16 | US-10-210-120-104 |
| 5          | 1146  | 100.0       | 2005      | 22 | US-10-909-035-104 |
| 6          | 1146  | 100.0       | 2069      | 9  | US-09-967-305-4   |
| 7          | 1146  | 100.0       | 2069      | 15 | US-10-205-823-17  |

*need print out*

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| 8  | 1132 | 98.8 | 3654 | 9  | US-09-967-305-6     | Sequence 6, Appli  |
| 9  | 1132 | 98.8 | 3654 | 15 | US-10-205-823-19    | Sequence 19, Appl  |
| 10 | 1095 | 95.5 | 2069 | 15 | US-10-205-823-25    | Sequence 25, Appl  |
| 11 | 1081 | 94.3 | 2626 | 15 | US-10-205-823-27    | Sequence 27, Appl  |
| 12 | 1070 | 93.4 | 1621 | 9  | US-09-759-143-107   | Sequence 107, App  |
| 13 | 1070 | 93.4 | 1621 | 9  | US-09-780-669-107   | Sequence 107, App  |
| 14 | 1070 | 93.4 | 1621 | 9  | US-09-030-606-107   | Sequence 107, App  |
| 15 | 1070 | 93.4 | 1621 | 9  | US-09-822-827-107   | Sequence 107, App  |
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| 18 | 1070 | 93.4 | 1621 | 9  | US-09-895-793-107   | Sequence 107, App  |
| 19 | 1070 | 93.4 | 1621 | 9  | US-09-895-814-107   | Sequence 107, App  |
| 20 | 1070 | 93.4 | 1621 | 13 | US-10-012-896-107   | Sequence 107, App  |
| 21 | 1070 | 93.4 | 1621 | 14 | US-10-010-940-107   | Sequence 107, App  |
| 22 | 1070 | 93.4 | 1621 | 16 | US-10-144-678A-107  | Sequence 107, App  |
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| 26 | 1070 | 93.4 | 2376 | 20 | US-10-357-930-21872 | Sequence 21872, A  |
| 27 | 1070 | 93.4 | 2376 | 20 | US-10-357-930-25228 | Sequence 25228, A  |
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| 30 | 797  | 63.5 | 1294 | 20 | US-10-357-930-22726 | Sequence 22726, A  |
| 31 | 797  | 63.5 | 1294 | 20 | US-10-357-930-27725 | Sequence 27725, A  |
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| 35 | 740  | 64.6 | 1316 | 15 | US-10-205-823-23    | Sequence 23, Appli |
| 36 | 595  | 51.9 | 2946 | 19 | US-10-205-823-29    | Sequence 29, Appli |
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| 38 | 595  | 51.9 | 3023 | 9  | US-09-967-305-8     | Sequence 8, Appli  |
| 39 | 595  | 51.9 | 3023 | 15 | US-10-205-823-21    | Sequence 21, Appli |
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#### ALIGNMENTS

RESULT 1  
US-09-967-305-3  
; Sequence 3, Application US/09967305  
; Patent No. US20020123081A1  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE  
; FILE REFERENCE: 07334-312001  
; CURRENT APPLICATION NUMBER: US/09/967,305  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/236,238  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1146  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1146)  
US-09-967-305-3  
Query Match 100.0%; Score 1146; DB 9; Length 1146;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 ATGGCATTGCGAGGATCTCGGTCTGTGAGCTGTCCGGCTCCCGCCCGGCTTCTGT 60  
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Db 61 GGTATGTCCTGGCTGACTTCGGGGGCGGTGATGACGGGAGCCGGGCTCCGGC 120  
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RESULT 2  
US-09-967-305-1  
; Sequence 1, Application US/09967305  
; Patent No. US20020123081A1  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE  
; FILE REFERENCE: 0734-312001  
; CURRENT APPLICATION NUMBER: US/09/967,305  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/236,238  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2005  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-967-305-1  
Query Match 100.0%; Score 1146; DB 9; Length 2005;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCATTGCGAGGATCTCGGTCTGTGAGCTGTCCGGCTCCCGCCCGGCTTCTGT 60  
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RESULT 3
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; Sequence 10, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE-
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1211)
US-09-967-305-10

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| Db | 126  | GCTATGGTCTCTGGCTGACTTCGGGGCCGGTGTGGTACCGCTGGACCCGGCCGGCTCCCGC     | 185  |
| QY | 121  | TACGACGTGAGCCGCTTGCGGGCCGGGGACAGCGCTCGCTAGTGTCTGACCTTGAAACGACCG   | 180  |
| Db | 186  | TACGACGTGAGCCGCTTGCGGGCCGGGGACAGCGCTCGCTAGTGTCTGACCTTGAAACGACCG   | 245  |
| QY | 181  | CGGGAGCCCGCGGTGTCTGGCGGTCTGTGCAAGCGGTCCGATGTGGTCTGGAGACCCCTTC     | 240  |
| Db | 246  | CGGGAGCCCGCGGTGTCTGGCGGTCTGTGCAAGCGGTCCGATGTGGTCTGGAGACCCCTTC     | 305  |
| QY | 241  | CGCGCGGGTGCATGAGAGAACTCCAGCTGGGGCCAGAGATTCGTGACGGGGAAATTC         | 300  |
| Db | 306  | CGCGCGGGTGCATGAGAGAACTCCAGCTGGGGCCAGAGATTCGTGACGGGGAAATTC         | 365  |
| QY | 301  | AGGCTTATTTATGCGCAGGCTGAGTGAGATTTGGCCAGCTCAGAGACCTTCGCGTTAGCT      | 360  |
| Db | 366  | AGGCTTATTTATGCGCAGGCTGAGTGAGATTTGGCCAGCTCAGAGACCTTCGCGTTAGCT      | 425  |
| QY | 361  | GGCCACCATATCACTATTTGGCTTTGGTCAGGTGTCTCTCAAAATTTGGAGAAAGGT         | 420  |
| Db | 426  | GGCCACCATATCACTATTTGGCTTTGGTCAGGTGTCTCTCAAAATTTGGAGAAAGGT         | 485  |
| QY | 421  | GAGAAATCCGTATGCCCCGCTGAATCTCCGTGCTACCTTGTGTGGTGGCTTATGTGT         | 480  |
| Db | 486  | GAGAAATCCGTATGCCCCGCTGAATCTCCGTGCTACCTTGTGTGGTGGCTTATGTGT         | 545  |
| QY | 481  | GCACCTGGGCAATTATATGCTCTTTTGTGACCGCACAGCACGCACTGGCAGAGGTCACTT      | 540  |
| Db | 546  | GCACCTGGGCAATTATATGCTCTTTTGTGACCGCACAGCACGCACTGGCAGAGGTCACTT      | 605  |
| QY | 541  | GATCGAATATATGATGAGAAAGGAAACAGCATTTTAAGTCTTTCTGTGGAAATTCAGAAA      | 600  |
| Db | 606  | GATCGAATATATGATGAGAAAGGAAACAGCATTTTAAGTCTTTCTGTGGAAATTCAGAAA      | 665  |
| QY | 601  | TCGAGTCTGTGGGAAACACTCGAGGACAGAAACGTGTGATGTGTGAGCACTTTCAT          | 660  |
| Db | 666  | TCGAGTCTGTGGGAAACACTCGAGGACAGAAACGTGTGATGTGTGAGCACTTTCAT          | 725  |
| QY | 661  | ACGACTTACAGACAGCAGATGGGGAAATTCATGCTGTGGAGCAATGCCACCTTC            | 720  |
| Db | 726  | ACGACTTACAGACAGCAGATGGGGAAATTCATGCTGTGGAGCAATGCCACCTTC            | 785  |
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| Db | 786  | TACAGAGCTGCATCAAAAGGACTTAAGTCTGATGTAACCTTCCCAATCAGATGAGC          | 845  |
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| Db | 846  | ATGATGATTTGGCCAGAAATGAAAGAGATTTGCAGATGTATTTGCAAGAGCGAAG           | 905  |
| QY | 841  | GCAGAGTGTGTCAATTCCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTGACTTT         | 900  |
| Db | 906  | GCAGAGTGTGTCAATTCCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTGACTTT         | 965  |
| QY | 901  | GAGAGGTTTTCATCATGATCAACAAGAGAAAGGGCTGTTTATACCAAGTAGAGAG           | 960  |
| Db | 966  | GAGAGGTTTTCATCATGATCAACAAGAGAAAGGGCTGTTTATACCAAGTAGAGAG           | 1025 |
| QY | 961  | CAGAGCTGAGACCCCGCCCTGCACTCTGTGTTTAAACACCCAGCCATCCCTTCTTTC         | 1020 |
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| QY | 1021 | AAAAGGATCTTTTATATGAGAAACACCTGAGAGATATCTTGAAAGATTTGGATTGAC         | 1080 |
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| QY | 1081 | CGCGAAGAGATTTATCAGCTTAACTCAATATAAATCTTGAAAGTAATTAAGGTAAAGCT       | 1140 |
| Db | 1146 | CGCGAAGAGATTTATCAGCTTAACTCAATATAAATCTTGAAAGTAATTAAGGTAAAGCT       | 1205 |

QY 1141 AGTCTC 1146  
 DB 1206 AGTCTC 1211

RESULT 4  
 US-10-210-120-104  
 ; Sequence 104, Application US/10210120  
 ; Publication No. US20030175736A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chinaiyan, Arul M.  
 ; APPLICANT: Rubin, Mark A.  
 ; APPLICANT: Steekumar, Arun  
 ; TITLE OF INVENTION: Expression Profile of Prostate Cancer  
 ; FILE REFERENCE: UM-07221  
 ; CURRENT FILING DATE: 2002-08-01  
 ; PRIOR FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: US 60/309,581  
 ; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 123  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 104  
 ; LENGTH: 2005  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-210-120-104

Query Match 100.0%; Score 1146; DB 16; Length 2005;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 GCTATGTCCTGCTGACTTCCGGGCGCGTGTGTAACGCGTGAACCGGCGCTCCCGC 120  
 DB 126 GCTATGTCCTGCTGACTTCCGGGCGCGTGTGTAACGCGTGAACCGGCGCTCCCGC 185  
 QY 121 TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTGCTGCTGGAAGCAAGCCG 180  
 DB 186 TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTGCTGCTGGAAGCAAGCCG 245  
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 DB 246 CGGGGAGCCGCGTGTGCGGCGTGTGCAAGCGGTGGATGTGCTGAGCCCTTC 305  
 QY 241 CGCCGCGGTGTGATGAGAGAACTCCAGCTGGGCCAGAGATTCTGCAAGCGGAAATCCA 300  
 DB 306 CGCCGCGGTGTGATGAGAGAACTCCAGCTGGGCCAGAGATTCTGCAAGCGGAAATCCA 365  
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 DB 366 AGGCTTATTATGACCAAGGCTGAGTGGATTGGCACTGAGAAAGCTTTCGCGTTAGCT 425  
 QY 361 GGCACGATATCAACTATTGGCTTGTGAGGTGTTCTCAAAAATTGGCAAGAGTGT 420  
 DB 426 GGCACGATATCAACTATTGGCTTGTGAGGTGTTCTCAAAAATTGGCAAGAGTGT 485  
 QY 421 GAGAAATCCGTATCCCGCTGATCTCTGCTGATCTTTCGCTGCTGCTGCTTATGT 480  
 DB 486 GAGAAATCCGTATCCCGCTGATCTCTGCTGATCTTTCGCTGCTGCTGCTTATGT 545  
 QY 481 GCATGGGCGATTAAATGAGCTCTTTTGAACCGCAACGCACTGGCAAGGCTCAGTCT 540  
 DB 546 GCATGGGCGATTAAATGAGCTCTTTTGAACCGCAACGCACTGGCAAGGCTCAGTCT 605  
 QY 541 GATGAAATATGATGAGAGCAAGCATATTTAAAGTTCTTCTGAGAAATCTCAGAA 600  
 DB 606 GATGAAATATGATGAGAGCAAGCATATTTAAAGTTCTTCTGAGAAATCTCAGAA 665

QY 601 TCGAGTCTGTGGAGACACTTCGAGACAGAAATGTTGGATGTGAGACACTTCTTAT 660  
 DB 666 TCGAGTCTGTGGAGACACTTCGAGACAGAAATGTTGGATGTGAGACACTTCTTAT 725  
 QY 661 ACGACTTACAGACAGCAAGATGGGAAATTCATGGCTGTGAGCAATGAAACCCAGTTC 720  
 DB 726 ACGACTTACAGACAGCAAGATGGGAAATTCATGGCTGTGAGCAATGAAACCCAGTTC 785  
 QY 721 TACGAGCTGCTGATCAAGACCTTGAAGTGAAGTGAAGTTCACATCAGATGAGC 780  
 DB 786 TACGAGCTGCTGATCAAGACCTTGAAGTGAAGTGAAGTTCACATCAGATGAGC 845  
 QY 781 ATGATGATGCGCCAGAAATGAGAAAGATTGCAATGTTTTCGAAAGACGAG 840  
 DB 846 ATGATGATGCGCCAGAAATGAGAAAGATTGCAATGTTTTCGAAAGACGAG 905  
 QY 841 GCAGAGTGTGTCAAATCTTTGAGCGGCAAGATGCTGTGAGACCTCGGTTCTGACTTT 900  
 DB 906 GCAGAGTGTGTCAAATCTTTGAGCGGCAAGATGCTGTGAGACCTCGGTTCTGACTTT 965  
 QY 901 GAGAGGTTGTTTCATCATGATCAACAAGAAAGGAGGCTGTTTATCAGCAGTGAAG 960  
 DB 966 GAGAGGTTGTTTCATCATGATCAACAAGAAAGGAGGCTGTTTATCAGCAGTGAAG 1025  
 QY 961 CAGAGCTGAGCCCGCCCTGACCTTCTGTTTAAACCCAGCCATCCCTTCTTTC 1020  
 DB 1026 CAGAGCTGAGCCCGCCCTGACCTTCTGTTTAAACCCAGCCATCCCTTCTTTC 1085  
 QY 1021 AAAAGGATCTTTCATGAGAGAAACACATGAGAGATTTGGAATTTGATTCAGC 1080  
 DB 1086 AAAAGGATCTTTCATGAGAGAAACACATGAGAGATTTGGAATTTGATTCAGC 1145  
 QY 1081 CGCGAAGATTTTACCTTACTCAGATTAATCATTTGAAAGTAAAGTAAAGCT 1140  
 DB 1146 CGCGAAGATTTTACCTTACTCAGATTAATCATTTGAAAGTAAAGTAAAGCT 1205  
 QY 1141 AGTCTC 1146  
 DB 1206 AGTCTC 1211

7200

RESULT 5  
 US-10-909-035-104  
 ; Sequence 104, Application US/10909035  
 ; Publication No. US20050136493A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rubin, Mark A.  
 ; APPLICANT: Chinaiyan, Arul M.  
 ; APPLICANT: Laxman, Bharathi  
 ; APPLICANT: Steekumar, Arun  
 ; TITLE OF INVENTION: AMACR Cancer Markers  
 ; FILE REFERENCE: UM-09098  
 ; CURRENT FILING DATE: 2004-07-30  
 ; NUMBER OF SEQ ID NOS: 123  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 104  
 ; LENGTH: 2005  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-909-035-104

Query Match 100.0%; Score 1146; DB 22; Length 2005;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGACAGGAGATCTCGGTCGTGAGCTGTCCGCTGGCCCGCGGCTTCTGT 60  
 DB 66 ATGGCACTGACAGGAGATCTCGGTCGTGAGCTGTCCGCTGGCCCGCGGCTTCTGT 125  
 QY 61 GCTATGTCCTGCTGACTTCCGGGCGCGTGTGTAACGCGTGAACCGGCGCTCCCGC 120  
 DB 126 GCTATGTCCTGCTGACTTCCGGGCGCGTGTGTAACGCGTGAACCGGCGCTCCCGC 185

QY 121 TACGACGTGAGCCGCTTGGGCGCGGCAAGCGCTCGTAGTGTGAGCCTGAAGCAGCCG 180  
DB 186 TACGACGTGAGCCGCTTGGGCGCGGCAAGCGCTCGTAGTGTGAGCCTGAAGCAGCCG 245  
QY 181 CGGGAGCCGCGCTGCTGCGGCGCTGTGTGCAAGCGGTGCGATGTGCTGCGAGCCCTTC 240  
DB 246 CGGGAGCCGCGCTGCTGCGGCGCTGTGTGCAAGCGGTGCGATGTGCTGCGAGCCCTTC 305  
QY 241 CGCGCGGTGTGATGAGAACTCCAGCTGGGCGCAAGATTCGTGAGCGGGAAATCCA 300  
DB 306 CGCGCGGTGTGATGAGAACTCCAGCTGGGCGCAAGATTCGTGAGCGGGAAATCCA 365  
QY 301 AGGCTATTATTCAGCAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 360  
DB 366 AGGCTATTATTCAGCAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 425  
QY 361 GCGCAGCATATCACTATTGTGCTGTGCTGAGTGTGCTGCAAAAATGGCAGAGTGT 420  
DB 426 GCGCAGCATATCACTATTGTGCTGTGCTGAGTGTGCTGCAAAAATGGCAGAGTGT 485  
QY 421 GAGATCCGTATGCCCCGCTGATCTCCGCTGAGCTTGGTGTGAGTGTGAGTGTGAGTGTGAGT 480  
DB 486 GAGATCCGTATGCCCCGCTGATCTCCGCTGAGCTTGGTGTGAGTGTGAGTGTGAGTGTGAGT 545  
QY 481 GCACTGGGATTTAATGCTCTTTTGAACGCGACAGCACTGGCAAGGGTCAGTCAAT 540  
DB 546 GCACTGGGATTTAATGCTCTTTTGAACGCGACAGCACTGGCAAGGGTCAGTCAAT 605  
QY 541 GATGCAAAATATGTGTGAGAGAACAGATATTAAATTTCTTTTCTGTGAGAAATCTAGAA 600  
DB 606 GATGCAAAATATGTGTGAGAGAACAGATATTAAATTTCTTTTCTGTGAGAAATCTAGAA 665  
QY 601 TCGAGTCTGTGGGAACACCTCGAGAGACAGAAATGTGTGAGTGTGAGTGTGAGTGTGAGT 660  
DB 666 TCGAGTCTGTGGGAACACCTCGAGAGACAGAAATGTGTGAGTGTGAGTGTGAGTGTGAGT 725  
QY 661 AGGACTTACAGGACAGACAGATGGGGAATTCATGGCTGTGAGCAATAGAACCCAGTTC 720  
DB 726 AGGACTTACAGGACAGACAGATGGGGAATTCATGGCTGTGAGCAATAGAACCCAGTTC 785  
QY 721 TACGACGTGCTGATCAAGAGACTTGTGACTTAAAGTGTGATGAACTTCCATCAGATGAG 780  
DB 786 TACGACGTGCTGATCAAGAGACTTGTGACTTAAAGTGTGATGAACTTCCATCAGATGAG 845  
QY 781 ATGATGATTTGGCAGAAATGAAAGAAAGTTTGCAGTGTATTGCAAGAAAGAGAG 840  
DB 846 ATGATGATTTGGCAGAAATGAAAGAAAGTTTGCAGTGTATTGCAAGAAAGAGAG 905  
QY 841 GCGAGCTGTGTCAAACTTTGACGCGACAGATGCGGTGTGCTCGGTTCTGACCTTT 900  
DB 906 GCGAGCTGTGTCAAACTTTGACGCGACAGATGCGGTGTGCTCGGTTCTGACCTTT 965  
QY 901 GAGAGTGTTCATCATGATCAACAAGAGAGCGGGCTCGTTTATCAACAGTGAAG 960  
DB 966 GAGAGTGTTCATCATGATCAACAAGAGAGCGGGCTCGTTTATCAACAGTGAAG 1025  
QY 961 GAGAGTGTGAGCCCGCTGCACTGTGCTTTAAACAACCCAGCCATCCTTCTTTTC 1020  
DB 1026 GAGAGTGTGAGCCCGCTGCACTGTGCTTTAAACAACCCAGCCATCCTTCTTTTC 1085  
QY 1021 AAAAGGATCTTTTCAATAGAGAACACATGAGAGATATCTTGAAGATTTGATTCAG 1080  
DB 1086 AAAAGGATCTTTTCAATAGAGAACACATGAGAGATATCTTGAAGATTTGATTCAG 1145  
QY 1081 CGGGAAGATTTATGAGCTTAATCAATGATTAATGATTAATGATTAATGATTAATGATTA 1140  
DB 1146 CGGGAAGATTTATGAGCTTAATCAATGATTAATGATTAATGATTAATGATTAATGATTA 1205  
QY 1141 AGTCTC 1146  
DB 1206 AGTCTC 1211

RESULT 6  
US-09-967-305-4  
; Sequence 4, Application US/09967305  
; Patent No. US20020123081A1  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE  
; FILE REFERENCE: 0734-312001  
; CURRENT APPLICATION NUMBER: US/09/967,305  
; PRIOR APPLICATION NUMBER: US 60/236,238  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (90)...(1235)  
US-09-967-305-4  
Query Match 100.0%; Score 1146; DB 9; Length 2069;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCACTGACAGGAGATCTCGGTGAGAGTGTGCGGCTGAGCCCGGAGCCGTTCTGT 60  
DB 90 ATGGCACTGACAGGAGATCTCGGTGAGAGTGTGCGGCTGAGCCCGGAGCCGTTCTGT 149  
QY 61 GCTATGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 120  
DB 150 GCTATGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 209  
QY 121 TACGACGTGAGCCGCTTGGGCGCGGCAAGCGCTCGTAGTGTGAGCCTGAAGCAGCCG 180  
DB 210 TACGACGTGAGCCGCTTGGGCGCGGCAAGCGCTCGTAGTGTGAGCCTGAAGCAGCCG 269  
QY 181 CGGGAGCCGCGGTGCTGCGGCTGTGCTGCAAGCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 240  
DB 270 CGGGAGCCGCGGTGCTGCGGCTGTGCTGCAAGCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 329  
QY 241 CGCGCGGTGTGATGAGAACTCCAGCTGGGCCAGAGATTTCTGACGCGGAAATCCA 300  
DB 330 CGCGCGGTGTGATGAGAACTCCAGCTGGGCCAGAGATTTCTGACGCGGAAATCCA 389  
QY 301 AGGCTATTATTCAGCAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 360  
DB 390 AGGCTATTATTCAGCAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 449  
QY 361 GCGCAGATATCACTATTGTGCTTGTGAGGTTCTGCAAAAATGGCAGAGTGT 420  
DB 450 GCGCAGATATCACTATTGTGCTTGTGAGGTTCTGCAAAAATGGCAGAGTGT 509  
QY 421 GAGAAATCCGTATGCCCCGCTGATCTCCGCTGAGCTTGTGCTGTGTGTGTGTGTGTGTGTGT 480  
DB 510 GAGAAATCCGTATGCCCCGCTGATCTCCGCTGAGCTTGTGCTGTGTGTGTGTGTGTGTGTGT 569  
QY 481 GCACTGGGATTTAATGCTCTTTTGAACGCGACAGCACTGGCAAGGTCAGTCAAT 540  
DB 570 GCACTGGGATTTAATGCTCTTTTGAACGCGACAGCACTGGCAAGGTCAGTCAAT 629  
QY 541 GATGCAAAATATGTGTGAGAGAACAGATATTAAATTTCTTTCTGTGAGAAATCTAGAA 600  
DB 630 GATGCAAAATATGTGTGAGAGAACAGATATTAAATTTCTTTCTGTGAGAAATCTAGAA 689  
QY 601 TCGAGTCTGTGGGAAGCACTCGAGAGACAGAAATGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 660  
DB 690 TCGAGTCTGTGGGAAGCACTCGAGAGACAGAAATGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 749

661 ACGACTTACAGACAGACAGATGGGAAATTCATGGCTGTGGACATAGAACCCAGTTTC 720  
DB ACGACTTACAGACAGACAGATGGGAAATTCATGGCTGTGGACATAGAACCCAGTTTC 809  
QY 721 TACGAGCTGCTATCAAGGACTTGGACTTAAGTCTGATGAATCTCCCATCAGATGAC 780  
DB 810 TACGAGCTGCTATCAAGGACTTGGACTTAAGTCTGATGAATCTCCCATCAGATGAC 869  
QY 781 ATGATGATGTGGCCAGAAATGAAGAAGATTGGAGATGATTTGGCAAGAAGACGAAG 840  
DB 870 ATGATGATGTGGCCAGAAATGAAGAAGATTGGAGATGATTTGGCAAGAAGACGAAG 929  
QY 841 GCAGAGTGTGTCAAAATCTTTTGCAGCGACAGATGCTGTGTGACTCCGGTTCTGACTTT 900  
DB 930 GCAGAGTGTGTCAAAATCTTTTGCAGCGACAGATGCTGTGTGACTCCGGTTCTGACTTT 989  
QY 901 GAGGAGTGTGTCAATCATATGATCAACAAGAAAGGAGGCTGTTTATCCACGTGAGAG 960  
DB 990 GAGGAGTGTGTCAATCATATGATCAACAAGAAAGGAGGCTGTTTATCCACGTGAGAG 1049  
QY 961 CAGGACGTGAGCCCGCCGCTGACCTGCTGTGTTAAACCCGACCCATCCCTCTTTC 1020  
DB 1050 CAGGACGTGAGCCCGCCGCTGACCTGCTGTGTTAAACCCGACCCATCCCTCTTTC 1109  
QY 1021 AAAAGGATCTTTTATAGAGAACACACTGAGAGATACCTTGAAGATTTGGATTCAAC 1080  
DB 1110 AAAAGGATCTTTTATAGAGAACACACTGAGAGATACCTTGAAGATTTGGATTCAAC 1169  
QY 1081 CGCGAAGATTTTATCACTTAATCACTCAATTAATATCAATTAAGTAAAGCT 1140  
DB 1170 CGCGAAGATTTTATCACTTAATCACTCAATTAATATCAATTAAGTAAAGCT 1229  
QY 1141 AGTCTC 1146  
DB 1230 AGTCTC 1235

RESULT 7  
US-10-205-823-17  
Sequence 17, Application US/10205823  
Publication No. US20030108963A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Endege, Wilson O.  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Gordatcheva, Bella  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Monsey, Angela M.  
APPLICANT: Glatt, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Anderson, Dustin  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
FILE REFERENCE: MRI-044  
CURRENT APPLICATION NUMBER: US/10/205,823  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,982  
PRIOR FILING DATE: 2001-07-25  
PRIOR APPLICATION NUMBER: 60/314,356  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/325,020  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 60/341,746  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/362,158  
PRIOR FILING DATE: 2002-03-05  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17

LENGTH: 2069  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-205-823-17

Query Match 100.0%; Score 1146; DB 15; Length 2069;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCACTGCAGAGGATCTCGGTGATGAGGCTGCTGGGCTGGGCGGCGGCTTCTGT 60  
DB 90 ATGGCACTGCAGAGGATCTCGGTGATGAGGCTGCTGGGCTGGGCGGCGGCTTCTGT 149  
QY 61 GCTATGCTCTGCTGACTTGGGCGGCTGTGTGTGACGCGTGAACCGGCGGCTCCGC 120  
DB 150 GCTATGCTCTGCTGACTTGGGCGGCTGTGTGTGACGCGTGAACCGGCGGCTCCGC 209  
QY 121 TACGACGTGAGCCGCTTGGGCGGCGCTGCTAGTGTGTGACCTTGAAGACGCC 180  
DB 210 TACGACGTGAGCCGCTTGGGCGGCGCTGCTAGTGTGTGACCTTGAAGACGCC 269  
QY 181 CGGGAGGCGCGGCTGCTGCGGCGTGTGTGCAAGGCGGTGAGTGTGCTGAGGCGCTTC 240  
DB 270 CGGGAGGCGCGGCTGCTGCGGCGTGTGTGCAAGGCGGTGAGTGTGCTGAGGCGCTTC 329  
QY 241 CGCGCGGTGTCTATGAGAAATCTCCAGCTGGGCGCCAGAGATTTGACAGCGGAAATCCA 300  
DB 330 CGCGCGGTGTCTATGAGAAATCTCCAGCTGGGCGCCAGAGATTTGACAGCGGAAATCCA 389  
QY 301 AGGCTTATTTATGCCAGGCTGATGTGATTTGGCCAGTCAAGAACTTTGCCCGTTAGCT 360  
DB 390 AGGCTTATTTATGCCAGGCTGATGTGATTTGGCCAGTCAAGAACTTTGCCCGTTAGCT 449  
QY 361 GGGCGAGATATCAATATTTGGCTTGTGAGGTGTCTCTCAAAATTTGGCAAGAGTGT 420  
DB 450 GGGCGAGATATCAATATTTGGCTTGTGAGGTGTCTCTCAAAATTTGGCAAGAGTGT 509  
QY 421 GAGAAATCCGTATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 510 GAGAAATCCGTATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569  
QY 481 GCACCTGGCATTTATATGCTCTTTTGAACGACACGCACTGGCAAGGCTCAGTCTT 540  
DB 570 GCACCTGGCATTTATATGCTCTTTTGAACGACACGCACTGGCAAGGCTCAGTCTT 629  
QY 541 GATCAAAATATGTGTGAGAAAGACGATTTAAGTCTTTTGTGTGAAAATCTGAGAA 600  
DB 630 GATCAAAATATGTGTGAGAAAGACGATTTAAGTCTTTTGTGTGAAAATCTGAGAA 689  
QY 601 TCGAGCTGTGGGAAGCACTCGAGAGACAAATGTTGATGTGTGAGCACTTTCTAT 660  
DB 690 TCGAGCTGTGGGAAGCACTCGAGAGACAAATGTTGATGTGTGAGCACTTTCTAT 749  
QY 661 ACGACTTACAGACAGACAGATGGGAAATTCATGCTGTGTGAGCAATAGAACCCAGTTTC 720  
DB 750 ACGACTTACAGACAGACAGATGGGAAATTCATGCTGTGTGAGCAATAGAACCCAGTTTC 809  
QY 721 TACGAGCTGCTATCAAGGACTTGGACTTAAGTCTGATGAATCTCCCATCAGATGAC 780  
DB 810 TACGAGCTGCTATCAAGGACTTGGACTTAAGTCTGATGAATCTCCCATCAGATGAC 869  
QY 781 ATGATGATGTGGCCAGAAATGAAGAAGATTGGAGATGATTTGGCAAGAAGACGAAG 840  
DB 870 ATGATGATGTGGCCAGAAATGAAGAAGATTGGAGATGATTTGGCAAGAAGACGAAG 929  
QY 841 GCAGAGTGTGTCAAAATCTTTTGCAGCGACAGATGCTGTGTGACTCCGGTTCTGACTTT 900  
DB 930 GCAGAGTGTGTCAAAATCTTTTGCAGCGACAGATGCTGTGTGACTCCGGTTCTGACTTT 989  
QY 901 GAGGAGTGTGTCAATCATATGATCAACAAGAAAGGAGGCTGTTTATCCACGTGAGAG 960  
DB 990 GAGGAGTGTGTCAATCATATGATCAACAAGAAAGGAGGCTGTTTATCCACGTGAGAG 1049

QY 961 CAGAGGTAGAGCCCGCCCTGACCTCTGCTTTAAACCCCGACATCCTCTTCTTC 1020  
DB 1050 CAGAGGTAGAGCCCGCCCTGACCTCTGCTTTAAACCCCGACATCCTCTTCTTC 1109  
QY 1021 AAAAGGATCTCTTCATAGAGAACACCTGAGAGATCTTGAAGATTTGGATTGACG 1080  
DB 1110 AAAAGGATCTCTTCATAGAGAACACCTGAGAGATCTTGAAGATTTGGATTGACG 1169  
QY 1081 CCGGAAGATTTATGAGCTTAACTGAGATTAATTAATTAAGTTAAAGCT 1140  
DB 1170 CCGGAAGATTTATGAGCTTAACTGAGATTAATTAATTAAGTTAAAGCT 1229  
QY 1141 AGCTTC 1146  
DB 1230 AGCTTC 1235

## RESULT 8

US-09-967-305-6  
Sequence 6, Application US/0967305  
Patent No. US20020123081A1  
GENERAL INFORMATION:  
APPLICANT: Richardson, Jennifer  
APPLICANT: Monahan, John  
TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-L-CA RACEMASE IN HORMONE  
FILE REFERENCE: 07334-312001  
CURRENT APPLICATION NUMBER: US/09/967,305  
CURRENT FILING DATE: 2001-09-28  
PRIOR APPLICATION NUMBER: US 60/236,238  
PRIOR FILING DATE: 2000-09-28  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 3654  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (90)...(1271)  
US-09-967-305-6

2

Query Match 98.8%; Score 1132; DB 9; Length 3654;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCACTGACGAGCATCTCGGTCTGAGAGCTGTCCGCGCTGCGCCCGCGCTTCTGT 60  
DB 90 ATGGCACTGACGAGCATCTCGGTCTGAGAGCTGTCCGCGCTGCGCCCGCGCTTCTGT 149  
QY 61 GGTATGCTCTGAGCTTGGGGGCGGTGTGTAAGCGGTGAGACCGCGCCGCTCCGCG 120  
DB 150 GGTATGCTCTGAGCTTGGGGGCGGTGTGTAAGCGGTGAGACCGCGCCGCTCCGCG 209  
QY 121 TACGACGTGAGCGCTTGGGCGCGGCGCAAGCGCTGCTGAGCTTGAAGAGCGCG 180  
DB 210 TACGACGTGAGCGCTTGGGCGCGGCGCAAGCGCTGCTGAGCTTGAAGAGCGCG 269  
QY 181 CCGGAGAGCGCGCTGCTGCGGCGGTCTGTGCAAGCGGTGAGTGTCTGTGAGCCCTTC 240  
DB 270 CCGGAGAGCGCGCTGCTGCGGCGGTCTGTGCAAGCGGTGAGTGTCTGTGAGCCCTTC 329  
QY 241 CCGCGGAGGTGATGAGAGAACTCCAGGCTGGGCGCAAGATCTGCAAGCGGAAATCCA 300  
DB 330 CCGCGGAGGTGATGAGAGAACTCCAGGCTGGGCGCAAGATCTGCAAGCGGAAATCCA 389  
QY 301 AGGCTTATTTATGACAGGCTGAGATTTGCGCAGTCAAGAGCTTCTGCGGTTAGCT 360  
DB 390 AGGCTTATTTATGACAGGCTGAGATTTGCGCAGTCAAGAGCTTCTGCGGTTAGCT 449  
QY 361 GCGCAGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAAGAGTGT 420  
DB 450 GCGCAGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAAGAGTGT 509

QY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGTGTGGCTTATGTGT 480  
DB 510 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGTGTGGCTTATGTGT 569  
QY 481 GCACTGGGATTTATATGCTCTTTTGAACGCAACGCACTGGCAAGGCTCAGTCAAT 540  
DB 570 GCACTGGGATTTATATGCTCTTTTGAACGCAACGCACTGGCAAGGCTCAGTCAAT 629  
QY 541 GATGCAATATGATGAGAGAAACAGATATTTAAAGTCTTTCTGTGAAAATCAGAAA 600  
DB 630 GATGCAATATGATGAGAGAAACAGATATTTAAAGTCTTTCTGTGAAAATCAGAAA 689  
QY 601 TCGAGCTGTGGGAGACACTTCAGAGACAGAACATGTTGATGTGAGACACTTTCTAT 660  
DB 690 TCGAGCTGTGGGAGACACTTCAGAGACAGAACATGTTGATGTGAGACACTTTCTAT 749  
QY 661 ACGACTTACAGACAGCAGATGAGGAAATTCATGCTGTTGAGCAATAGAACCCGATTC 720  
DB 750 ACGACTTACAGACAGCAGATGAGGAAATTCATGCTGTTGAGCAATAGAACCCGATTC 809  
QY 721 TACGAGCTGCTGATCAAGAGACTTGAATGATGAACTTCCCAATCAGATGAGC 780  
DB 810 TACGAGCTGCTGATCAAGAGACTTGAATGATGAACTTCCCAATCAGATGAGC 869  
QY 781 ATGATGATTTGGCCAGAAATGAAAGAGTTTGAGATGATTTGCAAGAGAGCAGAG 840  
DB 870 ATGATGATTTGGCCAGAAATGAAAGAGTTTGAGATGATTTGCAAGAGAGCAGAG 929  
QY 841 GCAAGGTGTCTCAATCTTTGACGCGCACAGATGCTGTGATCTCCGCTTCTGACTTTT 900  
DB 930 GCAAGGTGTCTCAATCTTTGACGCGCACAGATGCTGTGATCTCCGCTTCTGACTTTT 989  
QY 901 GAGAGGTTTGTTCATCATGATGATCAACAAGAGACCGGCTGTTTATCAACAGTGAAG 960  
DB 990 GAGAGGTTTGTTCATCATGATGATCAACAAGAGACCGGCTGTTTATCAACAGTGAAG 1049  
QY 961 CAGAGCTGAGCGCCCGCGCTGACCTGCTGCTTAAACCCCGACATCCTCTTCTTC 1020  
DB 1050 CAGAGCTGAGCGCCCGCGCTGACCTGCTGCTTAAACCCCGACATCCTCTTCTTC 1109  
QY 1021 AAAAGGATCTCTTCATAGAGAACACCTGAGAGATCTTGAAGATTTGGATTGACG 1080  
DB 1110 AAAAGGATCTCTTCATAGAGAACACCTGAGAGATCTTGAAGATTTGGATTGACG 1169  
QY 1081 CCGGAAGATTTATGAGCTTAACTGAGATTAATTAATTAAGTTAAAGCT 1140  
DB 1170 CCGGAAGATTTATGAGCTTAACTGAGATTAATTAATTAAGTTAAAGCT 1221

## RESULT 9

US-10-205-823-19  
Sequence 19, Application US/10205823  
Publication No. US20030108963A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Endege, Wilson O.  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Gorbacheva, Bella  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Kamakar, Shubhangi  
APPLICANT: Monney, Angela M.  
APPLICANT: Glatt, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Anderson, Duetlin  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
FILE REFERENCE: MRI-044  
CURRENT APPLICATION NUMBER: US/10/205, 823  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307, 982

&gt; 208-0

;; PRIOR FILING DATE: 2001-07-25  
;; PRIOR APPLICATION NUMBER: 60/314,356  
;; PRIOR FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/325,020  
;; PRIOR FILING DATE: 2001-09-25  
;; PRIOR APPLICATION NUMBER: 60/341,746  
;; PRIOR FILING DATE: 2001-12-12  
;; PRIOR APPLICATION NUMBER: 60/362,158  
;; PRIOR FILING DATE: 2002-03-05  
;; NUMBER OF SEQ ID NOS: 455  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO: 19  
;; LENGTH: 3654  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-205-823-19

Query Match 98.8%; Score 1132; DB 15; Length 3654;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAAGGATCTCGGTCGTGAGCTGTCGGCTGAGCCCGGGCCGGTTCTGT 60  
DB 90 ATGGCACTGCAAGGATCTCGGTCGTGAGCTGTCGGCTGAGCCCGGGCCGGTTCTGT 149  
QY 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 150 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209  
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
DB 210 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 269  
QY 181 CGGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 270 CGGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329  
QY 241 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 330 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389  
QY 301 AGGCTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 390 AGGCTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449  
QY 361 GCGCAAGATATCACTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
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QY 421 GAGAAATCCGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
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QY 481 GCACTGCGGCTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
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QY 601 TCGAGTCTGTGGAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
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DB 750 ACGACTTACAGGACAGCAGATGCGGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809  
QY 721 TACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
DB 810 TACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 869

QY 781 ATGATGATTTGCGCCAGAAATGAAAGAAAGTTTGCAATGTAATTTGCAAGAGACGAG 840  
DB 870 ATGATGATTTGCGCCAGAAATGAAAGAAAGTTTGCAATGTAATTTGCAAGAGACGAG 929  
QY 841 GCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
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DB 990 GAGAGCTTGTTCATCATGATACACAAAGAAAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049  
QY 961 CAGAGCTGAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
DB 1050 CAGAGCTGAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109  
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DB 1110 AAAAGGATTCCTTCATGAGAAACACCTGAGGAGATTAATTTGAAATTTGAAATTTGAA 1169  
QY 1081 CGCGAAGATTTATCACTTAATCACTGATTAATCACTGAAAGTAAATTAAG 1132  
DB 1170 CGCGAAGATTTATCACTTAATCACTGATTAATCACTGAAAGTAAATTAAG 1221

RESULT 10  
US-10-205-823-25  
; Sequence 25, Application US/10205823  
; Publication No. US20030108963A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Goebachere, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Womsey, Angela M.  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Duertin  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY FOR PROSTATE CANCER  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 25  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-823-25

Query Match 95.5%; Score 1095; DB 15; Length 2069;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAAGGATCTCGGTCGTGAGCTGTCGGCTGAGCCCGGGCCGGTTCTGT 60  
DB 90 ATGGCACTGCAAGGATCTCGGTCGTGAGCTGTCGGCTGAGCCCGGGCCGGTTCTGT 149

61 GCTATGTCCTGCTGATCTTCCGGGCGCGTGTGTAACGCTGAGACCGGCTCCGC 120  
150 GCTATGTCCTGCTGATCTTCCGGGCGCGTGTGTAACGCTGAGACCGGCTCCGC 209  
121 TACGAGTGAAGCGCTTGGGCGCGGCAAGCGCTGCTGATGCTGGAACCGGCGG 180  
210 TACGAGTGAAGCGCTTGGGCGCGGCAAGCGCTGCTGATGCTGGAACCGGCGG 269  
181 CCGGAGCGCGCGTGTGCGCGCTGTGCAAGCGCTGCTGATGCTGGAACCGGCTT 240  
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390 AGGCTATTATGCGCGCTGATGAGATTTGGCACTGAGAACTTTCCGCTTACGT 449  
361 GGCAGCATATCAACTATTTGGCTTGTGAGGTCTCTCAAAAATTTGGCAAGTGT 420  
450 GGCAGCATATCAACTATTTGGCTTGTGAGGTCTCTCTCAAAAATTTGGCAAGTGT 509  
421 GAGATCCGTATGCCCGCTGAACTCTGCGCTGACTTGTGTGTGTGTGTGTGT 480  
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481 GCACTGGGATATATATGCTCTTTTGAACCGCAACGCACTGGCAAGGTCAAGTCA 540  
570 GCACTGGGATATATATGCTCTTTTGAACCGCAACGCACTGGCAAGGTCAAGTCA 629  
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630 GATGCAATATATGCTGAGAAAGCAAGCACTATTTAAGTCTTTCTGTGAAAACTGAGAA 689  
601 TCGAGTCTGTGGAAAGCACTGAGGACAGAACTGTGTGATGTGTGAGCACTTTCTAT 660  
690 TCGAGTCTGTGGAAAGCACTGAGGACAGAACTGTGTGATGTGTGAGCACTTTCTAT 749  
661 AGCACTTACAGACAGCAAGTGGGAAATTCATGCTGTGTGAGCACTTTCTAT 720  
750 AGCACTTACAGACAGCAAGTGGGAAATTCATGCTGTGTGAGCACTTTCTAT 809  
721 TACGAGTGTCTGATCAAAAGCACTTGAAGTCTGATGAATCTTCCCAATCAGATGAGC 780  
810 TACGAGTGTCTGATCAAAAGCACTTGAAGTCTGATGAATCTTCCCAATCAGATGAGC 869  
781 ATGATGATGTGCGCAGAAATGAAGAAGATTTGCAATGATTTGCAAGAAGCAAG 840  
870 ATGATGATGTGCGCAGAAATGAAGAAGATTTGCAATGATTTGCAAGAAGCAAG 929  
841 GCAAGTGTGTCAAAATCTTTGACGCGCAGATGCTGTGTGATCTCCGCTTCTGACTTT 900  
930 GCAAGTGTGTCAAAATCTTTGACGCGCAGATGCTGTGTGATCTCCGCTTCTGACTTT 989  
901 GAGGAGTGTTCATCATGATGATCAACAAGGAAAGCGGCTGCTTTATCAGCAGTGAAG 960  
990 GAGGAGTGTTCATCATGATGATCAACAAGGAAAGCGGCTGCTTTATCAGCAGTGAAG 1049  
961 CAGGAGTGAAGCGCGCGCTGCACTTGTGTGTAACCGGCGGCTTCTTCTTCTTTC 1020  
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1021 AAAAGGATCTTTTATAGAGAACACTGAGAGATCTTGAAGAAATTTGATTCAGC 1080  
1110 AAAAGGATCTTTTATAGAGAACACTGAGAGATCTTGAAGAAATTTGATTCAGC 1169  
1081 CGCGAAGATTTATCAGCTTAACTCAGATTAATCATTTGAAAGTAAATTAAGTAAAGCT 1140  
1170 CGCGAAGATTTATCAGCTTAACTCAGATTAATCATTTGAAAGTAAATTAAGTAAAGCT 1229  
1141 AGTCTC 1146

Db 1230 AGTCTC 1235  
RESULT 11  
US-10-205-823-27  
; Sequence 27, Application US/10205823  
; Publication No. US20030108963A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gordatcheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kametkar, Shubhangi  
; APPLICANT: Womey, Angela M.  
; APPLICANT: Glatz, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Dustin  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TREATMENT OF PROSTATE CANCER  
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; PRIOR FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 2626  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-823-27  
Query Match 94.3%; Score 1081; DB 15; Length 2626;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 ATGGCACTGCAAGGATCTCGGTGTGAGGCTGTCGCGGCTTGGGCGCGGCTTCTGT 60  
90 ATGGCACTGCAAGGATCTCGGTGTGAGGCTGTCGCGGCTTGGGCGCGGCTTCTGT 149  
61 GCTATGTCCTGCTGATCTTCCGGGCGCGTGTGTAACGCTGAGACCGGCTCCGC 120  
150 GCTATGTCCTGCTGATCTTCCGGGCGCGTGTGTAACGCTGAGACCGGCTCCGC 209  
121 TACGAGTGAAGCGCTTGGGCGCGGCAAGCGCTGCTGATGCTGGAACCGGCGG 180  
210 TACGAGTGAAGCGCTTGGGCGCGGCAAGCGCTGCTGATGCTGGAACCGGCGG 269  
181 CCGGAGCGCGCGTGTGCGCGCTGTGCAAGCGCTGCTGATGCTGGAACCGGCTT 240  
270 CCGGAGCGCGCGTGTGCGCGCTGTGCAAGCGCTGCTGATGCTGGAACCGGCTT 329  
241 CCGCGCGGTGTGATGAGAACTCCAGCTGGGCGCGAGATTTGCAAGCGGAAATCCA 300  
330 CCGCGCGGTGTGATGAGAACTCCAGCTGGGCGCGAGATTTGCAAGCGGAAATCCA 389  
301 AGGCTATTATGCGCGCTGATGAGATTTGGCACTGAGAACTTTCCGCTTACGT 360  
390 AGGCTATTATGCGCGCTGATGAGATTTGGCACTGAGAACTTTCCGCTTACGT 449  
361 GGCAGCATATCAACTATTTGGCTTGTGAGGTCTCTCTCAAAAATTTGGCAAGTGT 420







|    |      |   |      |
|----|------|---|------|
| QY | 866  | GCACAGATCCCTGCTGATCTCCGGTCTCACTTTGAGAGGTTGATCATCATGATCAACA  | 925  |
| Db | 870  | GCACAGATCCCTGTGTGATCTCCGGTCTCACTTTGAGAGGTTGATCATCATGATCAACA | 929  |
| QY | 926  | ACAAGAAACGGGGCTTGTTATCACCACTGAGAGCAGGACGTCGCCGCCCTGCAC      | 985  |
| Db | 930  | ACAAAGAAACGGGGCTTGTTATCACCACTGAGAGCAGGACGTCGCCGCCCTGCAC     | 989  |
| QY | 986  | CTCTCTGTTAAACAACCCGAGCATCCCTCTTTCAAAGGGATCCCTTCATAGGAAAC    | 104  |
| Db | 990  | CTCTCTGTTAAACAACCCGAGCATCCCTCTTTCAAAGGGATCCCTTCATAGGAAAC    | 104  |
| QY | 1046 | ACACTGAGAGATTAAGATTTGATTCAGCCGCGAAGAGATTTACGCTTAAGT         | 110  |
| Db | 1050 | ACACTGAGAGATTAAGATTTGATTCAGCCGCGAAGAGATTTACGCTTAAGT         | 110  |
| QY | 1106 | CAGATAAATCAATGAAATTAATAGGTAAAGCTATGCTTC                     | 1146 |
| Db | 1110 | CAGATAAATCAATGAAATTAATAGGTAAAGCTATGCTTC                     | 1150 |

RESULT 13  
US-09-780-669-107  
; Sequence 107, Application US/09780665  
; Patent No. US2002005197A1 1  
; GENERAL INFORMATION:

```

1      APPLICANT: Xu, Jiangchun
2      APPLICANT: Dillon, Devin C.
3      APPLICANT: Mitcham, Jennifer L.
4      APPLICANT: Harlocker, Susan L.
5      APPLICANT: Uiang, Yuqiu
6      APPLICANT: Henderson, Robert A.
7      APPLICANT: Kalos, Michael D.
8      APPLICANT: Fanger, Gary R.
9      APPLICANT: Retter, Marc W.
10     APPLICANT: Stolk, John A.
11     APPLICANT: Day, Craig H.
12     APPLICANT: Vedvick, Thomas S.
13     APPLICANT: Carter, Darrick
14     APPLICANT: Li, Samuel
15     APPLICANT: Wang, Aijun
16     APPLICANT: Skeiky, Yasir A. W.
17     APPLICANT: Hepler, William
18     APPLICANT: Hurai, John
19     APPLICANT: McNeill, Patricia D.
20     APPLICANT: Houghton, Raymond L.
21     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
22     TITL OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
23     FILE REFERENCE: 210121.427C24
24     CURRENT APPLICATION NUMBER: US/09/780,669
25     CURRENT FILING DATE: 2001-02-09
26     NUMBER OF SEQ ID NOS: 943
27     SOFTWARE: FastSeq for Windows Version 3.0
28     SEQ ID NO 107
29     LENGTH: 1621
30     TYPE: DNA
31     ORGANISM: Homo sapien
32     US-09-780-669-107

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| Query Match           | 93.4%        | Score 1070  | DB 9         | Length 1621 |
| Best Local Similarity | 99.9%        | Pred. No. 0 |              |             |
| Matches 1120          | Conservative | 0           | Mismatches 1 | Indels 0    |
|                       |              |             | Gaps         | 0           |

  

|    |     |   |     |
|----|-----|---|-----|
| QY | 26  | TGAACTGTCCGGCCCTGGGCCCGGGGCCGTTCTGTGCTATATGAGCCGAGCTGAATTGGGG   | 85  |
| Db | 30  | TGGAGCTGTCCGGCCCTGGGCCCGGGGCCGTTCTGTGCTATATGAGCTGAATTGGGG       | 89  |
| QY | 86  | CGCGTGTGTGTACGCGGTGAGCCGGGCCCGGCTCCCGCTACACAGCTGAGCCGCTTGGGCGGG | 145 |
| Db | 90  | CGCGTGTGTGTACGCGGTGAGCCGGGCCCGGCTCCCGCTACAGACGTGAGCCGCTTGGGCGGG | 149 |
| QY | 146 | GCAAGCGCTCGCTAGTGTGTGAGCTTGAGACGACCGCGGGAGCCGCCGTGTGCGGCGTC     | 205 |

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|----|------|--|------|
| Db | 150  | GCAAGCGCTCGGTATGCTGTGACCTGAAAGCAGCCGCGGGGAGCCGCGCGTGTGGGCGCT   | 209  |
| Qy | 206  | TGTGCAGACCGGTCCGATGTGCTGCTGTGAGCCCTTCCGCGCGGTGTCAATGAGAAATCTCC | 265  |
| Db | 210  | TGTGCACACCGGTCCGATGTGCTGCTGTGAGCCCTTCCGCGCGGTGTCAATGAGAAATCTCC | 269  |
| Qy | 266  | AGCTGGGGCCAGAGATTTCTGACGGGGGAAAAATCCAAAGGCTTATTATGCAAGCTGAGTG  | 325  |
| Db | 270  | AGCTGGGGCCAGAGATTTCTGACGGGGGAAAAATCCAAAGGCTTATTATGCAAGCTGAGTG  | 329  |
| Qy | 326  | GATTTGGCCAGTCAGAGAGCTTCTGCGGGTATGCTGGCCAGATATCAATATTTGGCTT     | 385  |
| Db | 330  | GATTTGGCCAGTCAGAGAGCTTCTGCGGGTATGCTGGCCAGATATCAATATTTGGCTT     | 389  |
| Qy | 386  | TGTCAAGTGTCTCTCCAAAAATTTGGCAGAGATGTGTGAGATTCGATAGCCCGCTGATC    | 445  |
| Db | 390  | TGTCAAGTGTCTCTCCAAAAATTTGGCAGAGATGTGTGAGATTCGATAGCCCGCTGATC    | 449  |
| Qy | 446  | TCTGGGCTGACCTTGTCTGTGTGGCCCTTATGTGTGCACTGGGGCATTTAAATGGCTCTT   | 505  |
| Db | 450  | TCTGGGCTGACCTTGTCTGTGTGGCCCTTATGTGTGCACTGGGGCATTTAAATGGCTCTT   | 509  |
| Qy | 506  | TTGACCGCACAACGCACTGGCAGAGGTCAGGTCAATGATGCAATAATGTGTGAGAGACAG   | 565  |
| Db | 510  | TTGACCGCACAACGCACTGGCAGAGGTCAGGTCAATGATGCAATAATGTGTGAGAGACAG   | 569  |
| Qy | 566  | CATATTTAAGTCTTTTCTGTGTGAAAACTCAGAAATTCAGATCTGTGGGAGACCTCGAG    | 625  |
| Db | 570  | CATATTTAAGTCTTTTCTGTGTGAAAACTCAGAAATTCAGATCTGTGGGAGACCTCGAG    | 629  |
| Qy | 626  | GACAGAAATGTGGATGTGTGAGACCTTCTATAGCATTTACAGACATTAAGCAGATGGGG    | 685  |
| Db | 630  | GACAGAAATGTGGATGTGTGAGACCTTCTATAGCATTTACAGACATTAAGCAGATGGGG    | 689  |
| Qy | 686  | AATTCATGGCTGTGGAGCAATAGAACCCAGTTCTACAGCTGCTGATCAAAAGACCTTG     | 745  |
| Db | 690  | AATTCATGGCTGTGGAGCAATAGAACCCAGTTCTACAGCTGCTGATCAAAAGACCTTG     | 749  |
| Qy | 746  | GACTTAAATCTGTATGAATCTTCCCAATCAAGATGACATGATGATTTGGCCAGAAATGAGAC | 805  |
| Db | 750  | GACTTAAATCTGTATGAATCTTCCCAATCAAGATGACATGATGATTTGGCCAGAAATGAGAC | 809  |
| Qy | 806  | AGAAGTTTGCAGATGTATTTGCAAGAGAGACGAAAGGAGAGTGTGTAATCTTTGACG      | 865  |
| Db | 810  | AGAAGTTTGCAGATGTATTTGCAAGAGAGACGAAAGGAGAGTGTGTAATCTTTGACG      | 869  |
| Qy | 866  | GCAACGATGCCGTGTGTGACTCCGGTTCTGACTTTTGAAGAGGTGTTCATCATGATCA     | 925  |
| Db | 870  | GCAACGATGCCGTGTGTGACTCCGGTTCTGACTTTTGAAGAGGTGTTCATCATGATCA     | 929  |
| Qy | 926  | ACAAGAAACGGGGCTCTTTTATCACCAATGAGAGACAGAGATGAGCCCGCCCTGCAC      | 985  |
| Db | 930  | ACAAGAAACGGGGCTCTTTTATCACCAATGAGAGACAGAGATGAGCCCGCCCTGCAC      | 989  |
| Qy | 986  | CTGTGCTGTAAACACCCCAAGCATCCCTTCTTCAAAAAGGATCCCTTTCATAGGAGAC     | 1041 |
| Db | 990  | CTGTGCTGTAAACACCCCAAGCATCCCTTCTTCAAAAAGGATCCCTTTCATAGGAGAC     | 1044 |
| Qy | 1046 | ACACTGAGAGATATTTAAGAAATTTGGATTCAAGCCGGAAGAGATTTATCAGCTTAAT     | 1101 |
| Db | 1050 | ACACTGAGAGATATTTAAGAAATTTGGATTCAAGCCGGAAGAGATTTATCAGCTTAAT     | 1104 |
| Qy | 1106 | CAGATAAATCATTTGAAGTAATAAGTAAAGTAAAGCTATCTC 14746               |      |
| Db | 1110 | CAGATAAATCATTTGAAGTAATAAGTAAAGTAAAGCTATCTC 1150                |      |

RESULT 14  
US-09-030-606-107  
; Sequence 107, Application US/09030606  
; Patent No. US20020081580A1  
; GENERAL INFORMATION:





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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 05:32:03 ; Search time 230 Seconds  
(without alignments)  
8152.927 Million cell updates/sec

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Perfect score: 1146  
Sequence: 1 atggcactgcaggcatctc.....ataaggtaaagctagcttc 1146

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/ina/5B-COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A-COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | % Match | Query Length | DB ID | Description         |
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| 1          | 1142.8 | 99.7    | 1621         | 3     | US-09-020-956-107   |
| 2          | 1142.8 | 99.7    | 1621         | 3     | US-09-030-607-107   |
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| 4          | 1142.8 | 99.7    | 1621         | 3     | US-09-352-616A-107  |
| 5          | 1142.8 | 99.7    | 1621         | 3     | US-09-232-149A-107  |
| 6          | 1142.8 | 99.7    | 1621         | 4     | US-09-159-812-107   |
| 7          | 1142.8 | 99.7    | 1621         | 4     | US-09-636-215-107   |
| 8          | 1142.8 | 99.7    | 1621         | 4     | US-09-685-166A-107  |
| 9          | 1142.8 | 99.7    | 1621         | 4     | US-09-115-453-107   |
| 10         | 1142.8 | 99.7    | 1621         | 4     | US-09-688-489-107   |
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| 15         | 428.4  | 37.4    | 430          | 4     | US-09-736-457-1504  |
| 16         | 428.4  | 37.4    | 430          | 4     | US-09-614-124B-1504 |
| 17         | 428.4  | 37.4    | 430          | 4     | US-09-671-325-1504  |
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| 27         | 406.6  | 35.5    | 773          | 4     | US-09-115-453-3     |

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|------|-------|------|-----|---|-------------------|--------------------|
| C 28 | 406.6 | 35.5 | 773 | 4 | US-09-688-489-3   | Sequence 3, Appli  |
| C 29 | 406.6 | 35.5 | 773 | 4 | US-09-679-426-3   | Sequence 3, Appli  |
| C 30 | 406.6 | 35.5 | 773 | 4 | US-09-759-143-3   | Sequence 3, Appli  |
| C 31 | 406.6 | 35.5 | 773 | 4 | US-09-651-236-3   | Sequence 3, Appli  |
| C 32 | 403.2 | 35.2 | 793 | 3 | US-09-020-956-33  | Sequence 33, Appli |
| C 33 | 403.2 | 35.2 | 793 | 3 | US-09-030-607-33  | Sequence 33, Appli |
| C 34 | 403.2 | 35.2 | 793 | 3 | US-09-439-313-33  | Sequence 33, Appli |
| C 35 | 403.2 | 35.2 | 793 | 3 | US-09-352-616A-33 | Sequence 33, Appli |
| C 36 | 403.2 | 35.2 | 793 | 3 | US-09-232-149A-33 | Sequence 33, Appli |
| C 37 | 403.2 | 35.2 | 793 | 4 | US-09-159-812-33  | Sequence 33, Appli |
| C 38 | 403.2 | 35.2 | 793 | 4 | US-09-636-215-33  | Sequence 33, Appli |
| C 39 | 403.2 | 35.2 | 793 | 4 | US-09-685-166A-33 | Sequence 33, Appli |
| C 40 | 403.2 | 35.2 | 793 | 4 | US-09-115-453-33  | Sequence 33, Appli |
| C 41 | 403.2 | 35.2 | 793 | 4 | US-09-688-489-33  | Sequence 33, Appli |
| C 42 | 403.2 | 35.2 | 793 | 4 | US-09-679-426-33  | Sequence 33, Appli |
| C 43 | 403.2 | 35.2 | 793 | 4 | US-09-759-143-33  | Sequence 33, Appli |
| C 44 | 403.2 | 35.2 | 793 | 4 | US-09-651-236-33  | Sequence 33, Appli |
| C 45 | 400.2 | 34.9 | 816 | 3 | US-09-020-956-2   | Sequence 2, Appli  |

ALIGNMENTS

RESULT 1  
US-09-020-956-107  
; Sequence 107, Application US/09020956  
; Patent No. 6261562  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillin, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/020,956  
; FILING DATE: 09-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 107:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1621 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-09-020-956-107

Query Match 99.7%; Score 1142.8; DB 3; Length 1621;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCAGTGCAGGCATCTCGGTGAGCTGTGCGGCTGGCCCGGCGGCTTCTGT 60  
DB 5 ATGGCAGTGCAGGCATCTCGGTGAGCTGTGCGGCTGGCCCGGCGGCTTCTGT 64

QY 61 GCTATGGTCTGCTGACCTTGGGGCGCGTGTGGTACGCGTGAGCCGCCCGGCTCCCGC 120  
 Db 65 GCTATGGTCTGCTGACCTTGGGGCGCGTGTGGTACGCGTGAGCCGCCCGGCTCCCGC 124

QY 121 TACGACGTGAGCGCTTGGGGCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCGC 180  
 Db 125 TACGACGTGAGCGCTTGGGGCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCGC 184

QY 181 CGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTCTGCTGGAGCCCTTC 240  
 Db 185 CGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTCTGCTGGAGCCCTTC 244

QY 241 CGCCGGGTGTCATGGAGAACTCAGCTGGGCCAGAGATCTGCAGCGGGAATCCA 300  
 Db 245 CGCCGGGTGTCATGGAGAACTCAGCTGGGCCAGAGATCTGCAGCGGGAATCCA 304

QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGGTTAGCT 360  
 Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGGTTAGCT 364

QY 361 GGCACAGATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGGT 420  
 Db 365 GGCACAGATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGGT 424

QY 421 GAGAACTCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTGT 480  
 Db 425 GAGAACTCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTGT 484

QY 481 GCACCTGGGCAATTAATGGCTTTTGTACCGCACACGACCTGGCAAGGTCAGGTCAAT 540  
 Db 485 GCACCTGGGCAATTAATGGCTTTTGTACCGCACACGACCTGGCAAGGTCAGGTCAAT 544

QY 541 GATCAAAATATGGTGGAGAAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 600  
 Db 545 GATCAAAATATGGTGGAGAAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGAGACCTCGAGCAGACATGTTGGATGGTGGAGCCTTTCTAT 660  
 Db 605 TCGAGTCTGTGGAGACCTCGAGCAGACATGTTGGATGGTGGAGCCTTTCTAT 664

QY 661 ACAGCTTACAGCAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720  
 Db 665 ACAGCTTACAGCAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 724

QY 721 TACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780  
 Db 725 TACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGCCAGAAATGAGAGAGATTTGCGAGATGTTTGCAGAGACGAG 840  
 Db 785 ATGGATGATTGCCAGAAATGAGAGAGATTTGCGAGATGTTTGCAGAGACGAG 844

QY 841 CGAGAGTGTGTCAAACTTTTGCAGCAGCAGATGCTGTGTGACTCCGGTCTGACTTTT 900  
 Db 845 CGAGAGTGTGTCAAACTTTTGCAGCAGCAGATGCTGTGTGACTCCGGTCTGACTTTT 904

QY 901 GAGGAGGTGTTTCATCATGATCAACAAGAGAACCGGGCTCGTTTATCACCAGTGAGGAG 960  
 Db 905 GAGGAGGTGTTTCATCATGATCAACAAGAGAACCGGGCTCGTTTATCACCAGTGAGGAG 964

QY 961 CAGGAGGTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1020  
 Db 965 CAGGAGGTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1024

QY 1021 AAAAGGATCTTTTCAATAGGAAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1080  
 Db 1025 AAAAGGATCTTTTCAATAGGAAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1084

QY 1081 CGCGAAGAGATTTATCAGCTTAATCTCAGATAAAATCATTTGAAGTAATGAAGTAAAGCT 1140  
 Db 1085 CGCGAAGAGATTTATCAGCTTAATCTCAGATAAAATCATTTGAAGTAATGAAGTAAAGCT 1144

QY 1141 AGTCTC 1146  
 Db 1145 AGTCTC 1150

RESULT 2  
 US-09-030-607-107  
 ; Sequence 107, Application US/09030607  
 ; Patent No. 6262245  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
 ; NUMBER OF SEQUENCES: 224  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED and BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/09/030.607  
 ; FILING DATE: 25-FEB-1998  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Maki, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 210121.427C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 107:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1621 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; US-09-030-607-107

Query Match 99.7%; Score 1142.8; DB 3; Length 1621;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAAGGCACTCTCGGTCTGGAGCTGTCCGGCTGTGGCCCGGCGGCTTCGTGT 60  
 Db 5 ATGGCACTGCAAGGCACTCTCGGTCTGGAGCTGTCCGGCTGTGGCCCGGCGGCTTCGTGT 64

QY 61 GCTATGTCTTGGCTGACTTCGGGCGCGTGTGTACGCTGGACCGCGGCTCCCGC 120  
 Db 65 GCTATGTCTTGGCTGACTTCGGGCGCGTGTGTACGCTGGACCGCGGCTCCCGC 124

QY 121 TACGACGTGAGCGCTTGGGGCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCGC 180  
 Db 125 TACGACGTGAGCGCTTGGGGCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCGC 184

QY 181 CGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTCTGCTGGAGCCCTTC 240  
 Db 185 CGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTCTGCTGGAGCCCTTC 244

QY 241 CGCCGGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATCTGCAGCGGGAATCCA 300  
 Db 245 CGCCGGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATCTGCAGCGGGAATCCA 304

QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGGTTAGCT 360



Db 785 ATGGATGATGGCCAGAAATGAAGAAGTTTGAGATGATATTTGCAAGAGACGAAG 844  
QY 841 CGAGAGTGGTGTCAAAATCTTTGACGGGACAGATGCTGTGACATCCCGGTCTGACTTTT 900  
Db 845 CGAGAGTGGTGTCAAAATCTTTGACGGGACAGATGCTGTGACATCCCGGTCTGACTTTT 904  
QY 901 GAGGAGGTGTTCATCATGATCACAACAAGGAACGGGCTCGTTTATCACCAGTGAGGAG 960  
Db 905 GAGGAGGTGTTCATCATGATCACAACAAGGAACGGGCTCGTTTATCACCAGTGAGGAG 964  
QY 961 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTCTCTTC 1020  
Db 965 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTCTCTTC 1024  
QY 1021 AAAAGGATCTTTTCATAGGAGAAACACTGAGGAGATCTTGAAGAATTTGGATTCAGC 1080  
Db 1025 AAAAGGATCTTTTCATAGGAGAAACACTGAGGAGATCTTGAAGAATTTGGATTCAGC 1084  
QY 1081 CGCGAAGAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAGTAATAAGTAAAGCT 1140  
Db 1085 CGCGAAGAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAGTAATAAGTAAAGCT 1144  
QY 1141 AGTCTC 1146  
Db 1145 AGTCTC 1150

RESULT 4

US-09-352-616A-107

; Sequence 107, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang, Yuqui

; APPLICANT: Xu, Jiangchun

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.427C8

; CURRENT APPLICATION NUMBER: US/09/352,616A

; CURRENT FILING DATE: 1999-07-13

; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-352-616A-107

Query Match 99.7%; Score 1142.8; DB 3; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGGAGCTTCGGGCTGGCCCGGCGCCGCTCTGT 60  
Db 5 ATGGCACTGCAGGGCATCTCGTCTGGAGCTTCGGGCTGGCCCGGCGCCGCTCTGT 64  
QY 61 GTATGGTCTCGTCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGGCCCGGCTCCGCG 120  
Db 65 GCTATGGTCTCGTCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGGCCCGGCTCCGCG 124  
QY 121 TAGCAGCTGAGCGCTTGGCCCGGGGCAAGCGCTCGTAGTCTGAGACTGAAGCAGCGG 180  
Db 125 TAGCAGCTGAGCGCTTGGCCCGGGGCAAGCGCTCGTAGTCTGAGACTGAAGCAGCGG 184  
QY 181 CGGGAGCCCGCTGCTGCTGGGGCTGTCTCAAGCGGTGGATGCTGCTGAGCGCCCTTC 240  
Db 185 CGGGAGCCCGCTGCTGCTGGGGCTGTCTCAAGCGGTGGATGCTGCTGAGCGCCCTTC 244  
QY 241 CGCCGGGTGTATGAGAGAACTCCAGCTGGGCCAGAGATCTGCGAGCGGGAATCA 300

RESULT 5

US-09-232-149A-107

; Sequence 107, Application US/09232149A

; Patent No. 6465611

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

Db 245 CGCCGCGTGTATGAGAGAAATCCAGCTGGGCGCCAGAGATTTCTGACGGGGAATCCA 304  
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTTGGCCAGTCCAGAGCTTCTGCGGTTAGCT 360  
Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTTTGGCCAGTCCAGAGCTTCTGCGGTTAGCT 364  
QY 361 GGCCACGATATCAACTATTTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 420  
Db 365 GGCCACGATATCAACTATTTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 424  
QY 421 GAGAAATCCGATGCCCCGCTGAATCTCTGCTGCTGACTTTGTGCTGGTGGCTTATGTGT 480  
Db 425 GAGAAATCCGATGCCCCGCTGAATCTCTGCTGCTGACTTTGTGCTGGTGGCTTATGTGT 484  
QY 481 GCATCGGCGATTAATGCGCTCTTTTGGCCGACACGCACTGGCAAGGTCAGTCAAT 540  
Db 485 GCATCGGCGATTAATGCGCTCTTTTGGCCGACACGCACTGGCAAGGTCAGTCAAT 544  
QY 541 GATGCAATATGCTGGAGGAACAGCATATTTAAAGTCTTTTCTGTGAAAATCTCAGAAA 600  
Db 545 GATGCAATATGCTGGAGGAACAGCATATTTAAAGTCTTTTCTGTGAAAATCTCAGAAA 604  
QY 601 TCGAGTCTGTGGGAGCACTCGAGGACAGAAATGTTGGATGTTGGAGTGGTGGTCTTAT 660  
Db 605 TCGAGTCTGTGGGAGCACTCGAGGACAGAAATGTTGGATGTTGGAGTGGTGGTCTTAT 664  
QY 661 ACAGCTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720  
Db 665 ACAGCTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 724  
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Db 725 TACGAGTCTGTCAAAAGGACTTGGACTAAAGTCTGATGAATCTTCCCAATCAGATGAGC 784  
QY 781 ATGGATGATTCGCCAGAAATCAAGAAGATTTGCAGATGTATTTGCAAGAAAGACGAAG 840  
Db 785 ATGGATGATTCGCCAGAAATCAAGAAGATTTGCAGATGTATTTGCAAGAAAGACGAAG 844  
QY 841 CGAGAGTGGTCTCAATCTTTGACGGCACAGATGCTGTGACTTCCCGGTTCTGACTTTT 900  
Db 845 CGAGAGTGGTCTCAATCTTTGACGGCACAGATGCTGTGACTTCCCGGTTCTGACTTTT 904  
QY 901 GAGGAGGTGTTCATCATGATCACAACAAGGAAACGGGCTCGTTTATCACCAGTGAGGAG 960  
Db 905 GAGGAGGTGTTCATCATGATCACAACAAGGAAACGGGCTCGTTTATCACCAGTGAGGAG 964  
QY 961 CAGGACGTGAGCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTCTCTTC 1020  
Db 965 CAGGACGTGAGCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTCTCTTC 1024  
QY 1021 AAAAGGATCTTTTCATAGGAGAAACACTGAGGAGATCTTGAAGAATTTGGATTCAGC 1080  
Db 1025 AAAAGGATCTTTTCATAGGAGAAACACTGAGGAGATCTTGAAGAATTTGGATTCAGC 1084  
QY 1081 CGCGAAGAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAGTAATAAGTAAAGCT 1140  
Db 1085 CGCGAAGAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAGTAATAAGTAAAGCT 1144  
QY 1141 AGTCTC 1146  
Db 1145 AGTCTC 1150

RESULT 5

US-09-232-149A-107

; Sequence 107, Application US/09232149A

; Patent No. 6465611

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE



```
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-107

Query Match          99.7%; Score 1142.8; DB 3; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTCGAGGCAATCTCGTGTGGAGCTGTCCGGCTCGCCCCCGGCGCTTCTGT 60
DB 5 ATGGCACTCGAGGCAATCTCGTGTGGAGCTGTCCGGCTCGCCCCCGGCGCTTCTGT 64

QY 61 GCTATGGTCTCGCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGGCCGGCTCCGC 120
DB 65 GCTATGGTCTCGCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGGCCGGCTCCGC 124

QY 121 TACGACGTGAGCGGCTGTGGCGCGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCG 180
DB 125 TACGACGTGAGCGGCTGTGGCGCGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCG 184

QY 181 CGGGGAGCGCGCTGTGGCGGCTGTGTCAAGCGGTGCTGTGTGGAGCCCTTC 240
DB 185 CGGGGAGCGCGCTGTGGCGGCTGTGTCAAGCGGTGCTGTGTGGAGCCCTTC 244

QY 241 CGCGCGGTGTGATGAGAACTCGAGTGGCGCGGCAAGATTCGAGCGGGAATCCA 300
DB 245 CGCGCGGTGTGATGAGAACTCGAGTGGCGCGGCAAGATTCGAGCGGGAATCCA 304

QY 301 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCGCCGGTAGCT 360
DB 305 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCGCCGGTAGCT 364

QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAAGATGCT 420
DB 365 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAAGATGCT 424

QY 421 GAGATTCGATGCGCGCTGAATCTCTGGCTGACTTTGTGTGGTGGCTTTATGT 480
DB 425 GAGATTCGATGCGCGCTGAATCTCTGGCTGACTTTGTGTGGTGGCTTTATGT 484

QY 481 GCACTGGGATTTAATGCTCTTTTGGACGCGCACACGCTGGCAAGGTCAGGTCAAT 540
DB 485 GCACTGGGATTTAATGCTCTTTTGGACGCGCACACGCTGGCAAGGTCAGGTCAAT 544

QY 541 GATGCAAAATATGTTGGAAGAAACAGATATTTAAGTCTTTTCTGTGAAACTCAGAAA 600
DB 545 GATGCAAAATATGTTGGAAGAAACAGATATTTAAGTCTTTTCTGTGAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGAGACACTCGAGACAGAAACATGTTGGATGTGGAGCACTTTCTAT 660
DB 605 TCGAGTCTGTGGAGACACTCGAGACAGAAACATGTTGGATGTGGAGCACTTTCTAT 664

QY 661 ACAGCTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
DB 665 ACAGCTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 724

QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780
DB 725 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATGCGCAAGAAATGAAGAGATTTGAGATGTATTTGCAAGAGACGAG 840
DB 785 ATGGATGATGCGCAAGAAATGAAGAGATTTGAGATGTATTTGCAAGAGACGAG 844

QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
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DB 845 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTTGACTTTT 904
QY 901 GAGGAGGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACAGTGAGGAG 960
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DB 965 GAGGAGGTTGAGCCCGGCTTGACCTCTGCTGTTAAACACCCAGGCAATCCCTTCTTTC 1024
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DB 1025 AAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGATTCAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTTAACTCAGATAAAATCATTTGAAGTAATAAGGTAAAGCT 1140
DB 1085 CGCGAAGAGATTTATCAGCTTTAACTCAGATAAAATCATTTGAAGTAATAAGGTAAAGCT 1144
QY 1141 AGTCTC 1146
DB 1145 AGTCTC 1150

RESULT 6
US-09-159-812-107
; Sequence 107, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-107

Query Match          99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAAGGCAATCTCGTGTGGAGCTGTCCGGCTGGCCCCCGGCGCTTCTGT 60
DB 5 ATGGCACTGCAAGGCAATCTCGTGTATGAGAGCTGTCCGGCTGGCCCCCGGCGCTTCTGT 64

QY 61 GCTATGGTCTCGCTGACTTCGGGGCGGTGTGGTACCGGTGGACCGCGCGGCTCCGC 120
DB 65 GCTATGGTCTCGCTGACTTCGGGGCGGTGTGGTACCGGTGGACCGCGCGGCTCCGC 124

QY 121 TACGACGTGAGCGGCTGTGGCGCGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCG 180
DB 125 TACGACGTGAGCGGCTGTGGCGCGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCG 184

QY 181 CGGGGAGCGCGGTGTGCTGGCGGCTGTGTCAAGCGGTGCTGTGTGGAGCCCTTC 240
DB 185 CGGGGAGCGCGGTGTGCTGGCGGCTGTGTCAAGCGGTGCTGTGTGGAGCCCTTC 244

QY 241 CGCGCGGTGATGAGAACTCGAGTGGCGCGGCAAGATTCGAGCGGGAATCCA 300
DB 245 CGCGCGGTGATGAGAACTCGAGTGGCGCGGCAAGATTCGAGCGGGAATCCA 304

QY 301 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCGCCGGTAGCT 360
DB 305 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCGCCGGTAGCT 364

QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAAGATGCT 420
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Db 365 GGCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAGTGGT 424  
Qy 421 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTTATGTT 480  
Db 425 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTTATGTT 484  
Qy 481 GCATGGGCATTATATGCTCTTTTGAACCCACACGCACTGGCAAGGCTCAGTCAAT 540  
Db 485 GCATGGGCATTATATGCTCTTTTGAACCCACACGCACTGGCAAGGCTCAGTCAAT 544  
Qy 541 GATCAAAATATGGTGGAGGAAACAGATATTTAAAGTCTTTTCTGTGAAACTCAGAAA 600  
Db 545 GATCAAAATATGGTGGAGGAAACAGATATTTAAAGTCTTTTCTGTGAAACTCAGAAA 604  
Qy 601 TCGAGTCTGTGGAGACCTCGAGACAGACATGTTGGATGGTGGAGCACTTTCTAT 660  
Db 605 TCGAGTCTGTGGAGACCTCGAGACAGACATGTTGGATGGTGGAGCACTTTCTAT 664  
Qy 661 AGCACTTACAGACAGCAGATGGGAATTTCAATGGCTGTTGGAGCAATAGAACCCAGTTC 720  
Db 665 AGCACTTACAGACAGCAGATGGGAATTTCAATGGCTGTTGGAGCAATAGAACCCAGTTC 724  
Qy 721 TACGAGTCTGATCAAAAGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780  
Db 725 TACGAGTCTGATCAAAAGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 784  
Qy 781 ATGGATGATGGCCAGAAATGAAGAAGATTTGCAGATGATTTGCAAGNAGCAGAG 840  
Db 785 ATGGATGATTTGCCAGAAATGAAGAAGATTTGCAGATGATTTGCAAGNAGCAGAG 844  
Qy 841 CGAGAGTGTGTCAAAATCTTTCACGCGCACAGATGCTGTGACTCCGGTCTGACTTTT 900  
Db 845 CGAGAGTGTGTCAAAATCTTTCACGCGCACAGATGCTGTGACTCCGGTCTGACTTTT 904  
Qy 901 GAGGAGTGTGTTTCATCATGATCAACCAAGAAACGGGGCTCGTTTATCACAGTGAAGG 960  
Db 905 GAGGAGTGTGTTTCATCATGATCAACCAAGAAACGGGGCTCGTTTATCACAGTGAAGG 964  
Qy 961 CAGGAGTGAAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTTCTTC 1020  
Db 965 CAGGAGTGAAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTTCTTC 1024  
Qy 1021 AAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGATTCAGC 1080  
Db 1025 AAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGATTCAGC 1084  
Qy 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT 1140  
Db 1085 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT 1144  
Qy 1141 AGTCTC 1146  
Db 1145 AGTCTC 1150

RESULT 7

US-09-636-215-107  
; Sequence 107, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John H.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215  
; CURRENT FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 852  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-636-215-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCACTGACAGGCACTCTCGTCTGTGAGCTGTCCGGCTTGGCCCGGCGCCCTTCTGT 60  
Db 5 ATGCACTGACAGGCACTCTCGTCTGTGAGCTGTCCGGCTTGGCCCGGCGCCCTTCTGT 64  
Qy 61 GCTATGGTCTGCTGACTTCGGGCGCGTGTGTGACGCTGGACCGCCCGGCTCCCGC 120  
Db 65 GCTATGGTCTGCTGACTTCGGGCGCGTGTGTGACGCTGGACCGCCCGGCTCCCGC 124  
Qy 121 TACGACGTGAGCCGCTTTGGCGCGGCAAGCGCTCGTGTGAGCTGTGAGCTGTGAGCCG 180  
Db 125 TACGACGTGAGCCGCTTTGGCGCGGCAAGCGCTCGTGTGAGCTGTGAGCCG 184  
Qy 181 CGGAGGCGCGCTGCTCGCGCGTGTGTGCAAGCGGTGCGATGCTGTGAGCCCTTC 240  
Db 185 CGGAGGCGCGCTGCTCGCGCGTGTGTGCAAGCGGTGCGATGCTGTGAGCCCTTC 244  
Qy 241 CGCCGCGTGTCTGAGGAAATCTCAGCTGGCGCCAGAGATTTCTGACGCGGAAATCCA 300  
Db 245 CGCCGCGTGTCTGAGGAAATCTCAGCTGGCGCCAGAGATTTCTGACGCGGAAATCCA 304  
Qy 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360  
Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364  
Qy 361 GGCACGATATCAACTATTTGCTTGTGAGTGTCTCTCAAAATTTGGCAGAGTGGT 420  
Db 365 GGCACGATATCAACTATTTGCTTGTGAGTGTCTCTCAAAATTTGGCAGAGTGGT 424  
Qy 421 GAGATCCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGGTGGTGGCTTTATGTT 480  
Db 425 GAGATCCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGGTGGTGGCTTTATGTT 484  
Qy 481 GCATGGGCATTATATGCTCTTTTGAACCCACACGCACTGGCAAGGCTCAGTCAAT 540  
Db 485 GCATGGGCATTATATGCTCTTTTGAACCCACACGCACTGGCAAGGCTCAGTCAAT 544  
Qy 541 GATCAAAATATGGTGGAGGAAACAGATATTTAAAGTCTTTTCTGTGAAACTCAGAAA 600  
Db 545 GATCAAAATATGGTGGAGGAAACAGATATTTAAAGTCTTTTCTGTGAAACTCAGAAA 604  
Qy 601 TCGAGTCTGTGGAGACCTCGAGACAGACATGTTGGATGGTGGAGCACTTTCTAT 660  
Db 605 TCGAGTCTGTGGAGACCTCGAGACAGACATGTTGGATGGTGGAGCACTTTCTAT 664  
Qy 661 ACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720  
Db 665 ACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 724  
Qy 721 TACGAGTCTGATCAAAAGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780  
Db 725 TACGAGTCTGATCAAAAGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGCCGAAATGAAGAAAGTTTGCAGATGTATTTCRAAGAGCGAG 840  
Db |||||  
785 ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTCRAAGAGCGAG 844  
QY 841 GCAGAGTGTGTCAAAATCTTTGACCGGCACAGATGCTGTGTGACTCCGGTCTGTGACTTTT 900  
Db |||||  
845 GCAGAGTGTGTCAAAATCTTTGACCGGCACAGATGCTGTGTGACTCCGGTCTGTGACTTTT 904  
QY 901 GAGGAGTGTGTCAATCATCATGATCAACAAGAAAGCGGGCTCGTTTATCACAGTAGGAG 960  
Db |||||  
905 GAGGAGTGTGTCAATCATCATGATCAACAAGAAAGCGGGCTCGTTTATCACAGTAGGAG 964  
QY 961 CAGGAGTGTGTCAATCATCATGATCAACAAGAAAGCGGGCTCGTTTATCACAGTAGGAG 1020  
Db |||||  
965 CAGGAGTGTGTCAATCATCATGATCAACAAGAAAGCGGGCTCGTTTATCACAGTAGGAG 1024  
QY 1021 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACTTGAAGAATTTGGATTTCAGC 1080  
Db |||||  
1025 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACTTGAAGAATTTGGATTTCAGC 1084  
QY 1081 CCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAAATAAGGTAAAGCT 1140  
Db |||||  
1085 CCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAAATAAGGTAAAGCT 1144  
QY 1141 AGTCTC 1146  
Db |||||  
1145 AGTCTC 1150

## RESULT 8

US-09-685-166A-107

; Sequence 107, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C21

; CURRENT APPLICATION NUMBER: US/09/685,166A

; CURRENT FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 898

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-685-166A-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTCAGGGCATCTCGTGTGGAGCTGTCCGGCTCGCCCGCCGGCTTCTGT 60  
Db |||||  
5 ATGGCACTCAGGGCATCTCGTGTGGAGCTGTCCGGCTCGCCCGCCGGCTTCTGT 64  
QY 61 GCTATGCTCTGGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGGCCCGCTCCCGC 120

Db |||||  
65 GCTATGCTCTGGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGGCCCGCTCCCGC 124  
QY |||||  
121 TACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGCTAGTGTCTGGAACCTTGAAGCAGCGG 180  
Db |||||  
125 TACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGCTAGTGTCTGGAACCTTGAAGCAGCGG 184  
QY |||||  
181 CCGGAGAGCCGCTGCTGCGGGCTCTGTGCAAGCGGTGCGATGTCTGTGTGAGCCCTTTC 240  
Db |||||  
185 CCGGAGAGCCGCTGCTGCGGGCTCTGTGCAAGCGGTGCGATGTCTGTGTGAGCCCTTTC 244  
QY |||||  
241 CGCCCGGTGTATGAGAGAACTCCAGCTGGGCCAGAGATTTCTGACGGGGAATATCCA 300  
Db |||||  
245 CGCCCGGTGTATGAGAGAACTCCAGCTGGGCCAGAGATTTCTGACGGGGAATATCCA 304  
QY |||||  
301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCTGCCGGTGTAGCT 360  
Db |||||  
305 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCTGCCGGTGTAGCT 364  
QY |||||  
361 GGCACGATATCAACTATTTGGCTTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGTGT 420  
Db |||||  
365 GGCACGATATCAACTATTTGGCTTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGTGT 424  
QY |||||  
421 GAGATCCGATGATCCCGCTGAACTCTCTGGCTGACTTTGTGTGTGTGTGTGTGTGTGTGTGT 480  
Db |||||  
425 GAGATCCGATGATCCCGCTGAACTCTCTGGCTGACTTTGTGTGTGTGTGTGTGTGTGTGTGT 484  
QY |||||  
481 GCACCTGGGCAATTATTAATGGCTCTTTTTCACCGCACACGCACTGGCAAGGGTCAGGTCAATT 540  
Db |||||  
485 GCACCTGGGCAATTATTAATGGCTCTTTTTCACCGCACACGCACTGGCAAGGGTCAGGTCAATT 544  
QY |||||  
541 GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 600  
Db |||||  
545 GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 604  
QY |||||  
601 TCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660  
Db |||||  
605 TCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 664  
QY |||||  
661 ACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 720  
Db |||||  
665 ACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 724  
QY |||||  
721 TACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780  
Db |||||  
725 TACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 784  
QY |||||  
781 ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTCRAAGAGAGCGAG 840  
Db |||||  
785 ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTCRAAGAGAGCGAG 844  
QY |||||  
841 GCAGAGTGTGTCAAAATCTTTGACCGGCACAGATGCTGTGTGACTCCGGTCTGTGACTTTT 900  
Db |||||  
845 GCAGAGTGTGTCAAAATCTTTGACCGGCACAGATGCTGTGTGACTCCGGTCTGTGACTTTT 904  
QY |||||  
901 GAGGAGTGTGTTCATCATGATCAACAAGAAAGCGGGCTCGTTTATCACAGTAGGAG 960  
Db |||||  
905 GAGGAGTGTGTTCATCATGATCAACAAGAAAGCGGGCTCGTTTATCACAGTAGGAG 964  
QY |||||  
961 CAGGAGTGTGAGCCCGCCCGCTGACCTCTGTGTTTAAACACCCAGCCATCCCTTCTTTC 1020  
Db |||||  
965 CAGGAGTGTGAGCCCGCCCGCTGACCTCTGTGTTTAAACACCCAGCCATCCCTTCTTTC 1024  
QY |||||  
1021 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACTTGAAGAATTTGGATTTCAGC 1080  
Db |||||  
1025 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACTTGAAGAATTTGGATTTCAGC 1084  
QY |||||  
1081 CCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAATAAGGTAAAGCT 1140  
Db |||||  
1085 CCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAATAAGGTAAAGCT 1144  
QY |||||  
1141 AGTCTC 1146  
Db |||||

Db 1145 AGTCTC 1150

RESULT 9

US-09-115-453-107

; Sequence 107, Application US/09115453B

; Patent No. 6657056

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

; TITLE OF INVENTION: METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427C4

; CURRENT APPLICATION NUMBER: US/09/115,453B

; CURRENT FILING DATE: 1998-07-14

; NUMBER OF SEQ ID NOS: 228

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-115-453-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCTGGCCCCGGGCGCTTCTGT 60

Db 5 ATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCTGGCCCCGGGCGCTTCTGT 64

QY 61 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGGTACCGTGGACCGCGCGCTCCGCG 120

Db 65 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGGTACCGTGGACCGCGCGCTCCGCG 124

QY 121 TACGACGTGAGCGGCTTGGCGCGGCAAGCGCTCGCTAGTGTCTGAGCTGAAGCGCG 180

Db 125 TACGACGTGAGCGGCTTGGCGCGGCAAGCGCTCGCTAGTGTCTGAGCTGAAGCGCG 184

QY 181 CGGGAGCGCGCTGTGCGGCTCTGTGCAAGCGGTGGATGTCTGTGAGCGCTTC 240

Db 185 CGGGAGCGCGCTGTGCGGCTCTGTGCAAGCGGTGGATGTCTGTGAGCGCTTC 244

QY 241 CGCGCGGTGTCTATGGAGAACTCCAGCTGGCGCCAGAGATCTCAGCGGGAATCCA 300

Db 245 CGCGCGGTGTCTATGGAGAACTCCAGCTGGCGCCAGAGATCTCAGCGGGAATCCA 304

QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTTAGCT 360

Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTTAGCT 364

QY 361 GCGCAGATATCAATATTTGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAAAGTGT 420

Db 365 GCGCAGATATCAATATTTGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAAAGTGT 424

QY 421 GAGATCCGTATGCCCGCTGAATCTCCGCTGACTTGTGCTGGCTTATGT 480

Db 425 GAGATCCGTATGCCCGCTGAATCTCCGCTGACTTGTGCTGGCTTATGT 484

QY 481 GCACTGGGCAATTAATAGCTCTTTTGACCCGACACGCACTGGCAAGGCTCAGTCAAT 540

Db 485 GCACTGGGCAATTAATAGCTCTTTTGACCCGACACGCACTGGCAAGGCTCAGTCAAT 544

QY 541 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 600

Db 545 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGAGCACTCGAGGACACATGTTGGATGGTGGACCTTTCTAT 660

Db 605 TCGAGTCTGTGGAGCACTCGAGGACACATGTTGGATGGTGGACCTTTCTAT 664

QY 661 AGCACTTACAGGACAGCATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 720

Db 665 ACGACTTACAGGACAGCAGATGGGAAATTCATGCTCTGTGGAGCAATAGAACCCAGTTC 724

QY 721 TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780

Db 725 TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAAAGAACGAAAG 840

Db 785 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAAAGAACGAAAG 844

QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900

Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 904

QY 901 GAGGAGTGTTCATCATGATCAACAAGAAAGCGGCTCGTTTATCACCAGTGAAGGAG 960

Db 905 GAGGAGTGTTCATCATGATCAACAAGAAAGCGGCTCGTTTATCACCAGTGAAGGAG 964

QY 961 CAGGACGTGAGCGCCCGCTTCACTGCTGTGTTAAACACCCAGCCATCCCTTTCTTC 1020

Db 965 CAGGACGTGAGCGCCCGCTTCACTGCTGTGTTAAACACCCAGCCATCCCTTTCTTC 1024

QY 1021 AAAAGGATCTTTCTATAGAGAAACACACTGAGGAGATCTTGAAGATTTGGATTGAGC 1080

Db 1025 AAAAGGATCTTTCTATAGAGAAACACACTGAGGAGATCTTGAAGATTTGGATTGAGC 1084

QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAAATAGGTAAAGCT 1140

Db 1085 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAAATAGGTAAAGCT 1144

QY 1141 AGTCTC 1146

Db 1145 AGTCTC 1150

RESULT 10

US-09-688-489-107

; Sequence 107, Application US/09688489

; Patent No. 6664377

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Micham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427D2

; CURRENT APPLICATION NUMBER: US/09/688,489

; CURRENT FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-688-489-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCTGGCCCCGGGCGCTTCTGT 60

Db 5 ATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCTGGCCCCGGGCGCTTCTGT 64

QY 61 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGGTACCGTGGACCGCGCGCTCCGCG 120

Db 65 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGGTACCGTGGACCGCGCGCTCCGCG 124

QY 121 TACGACGTGAGCGGCTTGGCGCGGCAAGCGCTCGCTAGTGTCTGAGCTGAAGCGCG 180

Db 125 TACGACGTGAGCGGCTTGGCGCGGCAAGCGCTCGCTAGTGTCTGAGCTGAAGCGCG 184

QY 181 CGGGAGCGCGCTGTGCGGCTCTGTGCAAGCGGTGGATGTCTGTGAGCGCTTC 240

185 CGGGAGCGCGTGTGCGGCTCTGTGCAAGCGTGGATGTGCTGTGAGCCCTTC 244  
241 CGCGCGGTGTCTATGAGAAATCCAGCTGGGCCCAGAGATTCGAGCGGGAATCCA 300  
245 CGCGCGGTGTCTATGAGAAATCCAGCTGGGCCCAGAGATTCGAGCGGGAATCCA 304  
301 AGGCTTATTTATGCGAGGCTGAGTGATTTGGCAGTCAGAGCTTCGCGGTAGCT 360  
305 AGGCTTATTTATGCGAGGCTGAGTGATTTGGCAGTCAGAGCTTCGCGGTAGCT 364  
361 GGCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTCGAGAGTGT 420  
365 GGCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTCGAGAGTGT 424  
421 GAGATCCGATATGCCCCGCTGATCTCTGGCTGACTTTGCTGGTGGCTTATGTGT 480  
425 GAGATCCGATATGCCCCGCTGATCTCTGGCTGACTTTGCTGGTGGCTTATGTGT 484  
481 GCAGTGGCATTTATATGCTCTTTTGGACCGCAGCAGCTGGCAGGCTCAGGTCAAT 540  
485 GCAGTGGCATTTATATGCTCTTTTGGACCGCAGCAGCTGGCAGGCTCAGGTCAAT 544  
541 GATGCAATATGCTGGAAGGAAACAGCATATTTAAGTTCTTTCTGTGGAATCAGAA 600  
545 GATGCAATATGCTGGAAGGAAACAGCATATTTAAGTTCTTTCTGTGGAATCAGAA 604  
601 TCGAGTCTGTGGAGACACCTCGAGCAGAGACATGTTGGATGGTGGAGCCTTCTAT 660  
605 TCGAGTCTGTGGAGACACCTCGAGCAGAGACATGTTGGATGGTGGAGCCTTCTAT 664  
661 AGCACTTACAGACAGCAGATGGGAAATTCATGGCTTTGGAGCAATAGAACCCAGTTC 720  
665 AGCACTTACAGACAGCAGATGGGAAATTCATGGCTTTGGAGCAATAGAACCCAGTTC 724  
721 TACGAGCTCTGATCAAGGACTTGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780  
725 TACGAGCTCTGATCAAGGACTTGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGC 784  
781 ATGGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATTTTGCAGAAAGACGAG 840  
785 ATGGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATTTTGCAGAAAGACGAG 844  
841 GCAGAGTGTGCAATCTTTGACGCGCAGATGCTGTGCACTCCGCTCTGACTTTT 900  
845 GCAGAGTGTGCAATCTTTGACGCGCAGATGCTGTGCACTCCGCTCTGACTTTT 904  
901 GAGGAGTGTTCATCATGATCACAACAGGAAACGCGGCTCGTTTATCACCAGTGGAG 960  
905 GAGGAGTGTTCATCATGATCACAACAGGAAACGCGGCTCGTTTATCACCAGTGGAG 964  
961 CAGGAGCTGAGCCCCCGCTGCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1020  
965 CAGGAGCTGAGCCCCCGCTGCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1024  
1021 AAAAGGATTCCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1080  
1025 AAAAGGATTCCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1084  
1081 CCGGAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAATAGGTAAGCT 1140  
1085 CCGGAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAATAGGTAAGCT 1144  
1141 AGTCTC 1146  
1145 AGTCTC 1150

RESULT 11  
US-09-679-426-107  
; Sequence 107, Application US/09679426  
; Patent No. 6759515  
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqui  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, William  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C20  
CURRENT APPLICATION NUMBER: US/09/679,426  
CURRENT FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 895  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 107  
LENGTH: 1621  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-679-426-107  
Query Match 99.7%; Score 1142.8; DB 4; Length 1621;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCTGCGCCCGGCCCGCTTCGT 60  
DB 5 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCTGCGCCCGGCCCGCTTCGT 64  
QY 61 GCTATGTCCTGGCTGACTTCGGGGCGGTGTGGTACGCTGGACCGCGCCGGCTCCCGC 120  
DB 65 GCTATGTCCTGGCTGACTTCGGGGCGGTGTGGTACGCTGGACCGCGCCGGCTCCCGC 124  
QY 121 TACGACGTGAGCGCTTCGGGCGGCGCAAGCGCTCGCTAGTCTGGAAGCAGCGC 180  
DB 125 TACGACGTGAGCGCTTCGGGCGGCGCAAGCGCTCGCTAGTCTGGAAGCAGCGC 184  
QY 181 CGGGAGCGCGGCTGCTGCGGCTGTGCAAGCGGTGGATGCTGCTGAGAGCCCTTC 240  
DB 185 CGGGAGCGCGGCTGCTGCGGCTGTGCAAGCGGTGGATGCTGCTGAGAGCCCTTC 244  
QY 241 CGCGCGGTGTCTATGAGAAATCCAGCTGGGCCCAGAGATTCGAGCGGGAATCCA 300  
DB 245 CGCGCGGTGTCTATGAGAAATCCAGCTGGGCCCAGAGATTCGAGCGGGAATCCA 304  
QY 301 AGGCTTATTTATGCGAGGCTGAGTGGAATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 360  
DB 305 AGGCTTATTTATGCGAGGCTGAGTGGAATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 364  
QY 361 GGCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAGTGT 420  
DB 365 GGCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAGTGT 424  
QY 421 GAGATCCGATATGCCCCGCTGAAATCTCTGCTGCTGACTTTGCTGGTGGCTTATGTGT 480  
DB 425 GAGATCCGATATGCCCCGCTGAAATCTCTGCTGCTGACTTTGCTGGTGGCTTATGTGT 484  
QY 481 GCAGTGGCATTTATATGCTCTTTTGGACCGCAGCAGCTGGCAGGCTCAGGTCAAT 540  
DB 485 GCAGTGGCATTTATATGCTCTTTTGGACCGCAGCAGCTGGCAGGCTCAGGTCAAT 544  
QY 541 GATGCAATATGCTGGAAGGAAACAGCATATTTAAGTTCTTTCTGTGGAATCAGAA 600  
DB 545 GATGCAATATGCTGGAAGGAAACAGCATATTTAAGTTCTTTCTGTGGAATCAGAA 604

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QY 601 TCGAGTCTGTGGGAGACACCTCGAGGACAGAAACATGTTGGATGTTGGAGGACCTTTCTAT 660
Db 605 TCGAGTCTGTGGGAGACACCTCGAGGACAGAAACATGTTGGATGTTGGAGGACCTTTCTAT 664
QY 661 ACAGCTTACAGACAGCAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTC 720
Db 665 ACAGCTTACAGACAGCAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGTCTGTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780
Db 725 TACGAGTCTGTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGATGAGC 784
QY 781 ATGATGATGTCGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAAAGAACGAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAAAGAACGAG 844
QY 841 GCAGAGTGTGTCAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTATCACCAGTGAGGAG 964
QY 961 CAGGAGTGTAGCCCGCCCTGCACCTCTGTGTTTAAACACCCAGCCATCCCTTTTTC 1020
Db 965 CAGGAGTGTAGCCCGCCCTGCACCTCTGTGTTTAAACACCCAGCCATCCCTTTTTC 1024
QY 1021 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATTTCAGC 1080
Db 1025 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATTTCAGC 1084
QY 1081 CSCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTGAAGTAATAAGTAAAGCT 1140
Db 1085 CSCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTGAAGTAATAAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

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RESULT 12
US-09-759-143-107
; Sequence 107, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621

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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-107
Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCGACTGAGGGCATCTCGTCTGTGAGCTGTCCGGCTTGGCCCGGCGCCCTTCTGT 60
Db 5 ATGCGACTGAGGGCATCTCGTCTGTGAGCTGTCCGGCTTGGCCCGGCGCCCTTCTGT 64
QY 61 GCTATGCTCTGCTGCTGCTTGGGCGCGGCAAGCGCTCGCTAGTGTGGAACCTGAAACGAGCG 120
Db 65 GCTATGCTCTGCTGCTGCTTGGGCGCGGCAAGCGCTCGCTAGTGTGGAACCTGAAACGAGCG 124
QY 121 TACGACCTGAGCCCTTGGGCGCGGCAAGCGCTCGCTAGTGTGGAACCTGAAACGAGCG 180
Db 125 TACGACCTGAGCCCTTGGGCGCGGCAAGCGCTCGCTAGTGTGGAACCTGAAACGAGCG 184
QY 181 CGGGAGCGCGCTGTGCTGCGGCTGTGTGCAAGCGGTCGATGTGCTGCTGGAGCCCTTC 240
Db 185 CGGGAGCGCGCTGTGCTGCGGCTGTGTGCAAGCGGTCGATGTGCTGCTGGAGCCCTTC 244
QY 241 CGCGCGGTGTTCATGGAGAACTCCAGCTGGGCGCAGAGATTTCTGCAGCGGAAATCCA 300
Db 245 CGCGCGGTGTTCATGGAGAACTCCAGCTGGGCGCAGAGATTTCTGCAGCGGAAATCCA 304
QY 301 AGGCTTATTTATGTCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db 305 AGGCTTATTTATGTCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAGTGT 420
Db 365 GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAGTGT 424
QY 421 GAGATCGTATGCTCCGCTGAATCTCTGCTGCTGACTTGTGCTGGTGGGCTTATGCT 480
Db 425 GAGATCGTATGCTCCGCTGAATCTCTGCTGCTGACTTGTGCTGGTGGGCTTATGCT 484
QY 481 GCACCTGGGCATTATAATGGCTCTTTTGAACGCGCACGCACTGGCAAGGGTCAGTCAAT 540
Db 485 GCACCTGGGCATTATAATGGCTCTTTTGAACGCGCACGCACTGCAAGGGTCAGTCAAT 544
QY 541 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAGTCTTTTCTGTGCAAAACTCAGAA 600
Db 545 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAGTCTTTTCTGTGCAAAACTCAGAA 604
QY 601 TCGAGTCTGTGGAGGACCTCGAGGACAGAACTGTTGGATGGTGGAGCAGCTTTCTAT 660
Db 605 TCGAGTCTGTGGAGGACCTCGAGGACAGAACTGTTGGATGGTGGAGCAGCTTTCTAT 664
QY 661 ACAGCTTACAGACAGCAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTC 720
Db 665 ACAGCTTACAGACAGCAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGTCTGTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780
Db 725 TACGAGTCTGTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGATTTTGAAGAAAGAACGAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGATTTTGAAGAAAGAACGAG 844
QY 841 GCAGAGTGTGTCAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTATCACCAGTGAGGAG 964
QY 961 CAGGAGTGTAGCCCGCCCTGCACCTCTGTGTTTAAACACCCAGCCATCCCTTTTTC 1020

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Db 965 CAGGAGCTGAGCCGCCCTGACCTCTGCTGTATAACCCAGCCATCCCTTCTTC 1024  
Qy 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTCAGC 1080  
Db 1025 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTCAGC 1084  
Qy 1081 CGGAGAGATTTTATCAGCTTAATCTAGATATAAATCATTTGAAGTAATAAGGTAAAGCT 1140  
Db 1085 CGGAGAGATTTTATCAGCTTAATCTAGATATAAATCATTTGAAGTAATAAGGTAAAGCT 1144  
Qy 1141 AGTCTC 1146  
Db 1145 AGTCTC 1150

## RESULT 13

US-09-651-236-107

; Sequence 107, Application US/09651236

; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-651-236-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCACTGAGGACATCTCGGTGCTGAGAGCTGTCGGCCCTGCGCCCGGCCCTTCTGT 60

Db 5 ATGGCACTGAGGACATCTCGGTGCTGAGAGCTGTCGGCCCTGCGCCCGGCCCTTCTGT 64

Qy 61 GCTATGCTCTGCTGACTTTCGGGGCGCGTGTGTGCTGAGACCGGCCCGGCCCTCCGC 120

Db 65 GCTATGCTCTGCTGACTTTCGGGGCGCGTGTGTGCTGAGACCGGCCCGGCCCTCCGC 124

Qy 121 TAGACCTGAGCCGCTTGGCCCGGGCAAGCGTCTCGTGTGCTTGGACCTGGAAGCAGCCG 180

Db 125 TAGACCTGAGCCGCTTGGCCCGGGCAAGCGTCTCGTGTGCTTGGACCTGGAAGCAGCCG 184

Qy 181 CGGGAGCCCGCGTGTCTGTCGCGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 240

Db 185 CGGGAGCCCGCGTGTCTGTCGCGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 244

Qy 241 CGGGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTTCTGACGCGGGAAATCCA 300

## RESULT 14

US-09-702-705-1504

; Sequence 1504, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom



```
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1504
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1504

Query Match      37.4%; Score 428.4; DB 4; Length 430;
Best Local Similarity 99.8%; Pred. No. 1.5e-122;
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 363 CCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGGTGA 422
Db 1 CCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGGTGA 60

QY 423 GAATCCGATATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTTATGTGTC 482
Db 61 GAATCCGATATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTTATGTGTC 120

QY 483 ACTGGGCATTATTAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGTCAATTGA 542
Db 121 ACTGGGCATTATTAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGTCAATTGA 180

QY 543 TGCATAATATGGTGGAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAGAACTCAGAAATC 602
Db 181 TGCATAATATGGTGGAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAGAACTCAGAAATC 240

QY 603 GAGTCTGTGGGAGACACCTCGAGGACAGAACATGTTGGATGGTGGAGCAATAGAACCCAGTTCTA 722
Db 241 GAGTCTGTGGGAGACACCTCGAGGACAGAACATGTTGGATGGTGGAGCAATAGAACCCAGTTCTA 300

QY 663 GACTTACAGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTCTA 722
Db 301 GACTTACAGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTCTA 360

QY 723 CGAGCTGCTGATCAAGAGCTTGGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGCAT 782
Db 361 CGAGCTGCTGATCAAGAGCTTGGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGCAT 420

QY 783 GGATGATTGG 792
Db 421 GGATGATTGG 430
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## RESULT 15

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US-09-736-457-1504
; Sequence 1504, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, AiJun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
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; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1504
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1504

Query Match      37.4%; Score 428.4; DB 4; Length 430;
Best Local Similarity 99.8%; Pred. No. 1.5e-122;
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 363 CCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGGTGA 422
Db 1 CCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGGTGA 60

QY 423 GAATCCGATATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTTATGTGTC 482
Db 61 GAATCCGATATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTTATGTGTC 120

QY 483 ACTGGGCATTATTAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGTCAATTGA 542
Db 121 ACTGGGCATTATTAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGTCAATTGA 180

QY 543 TGCATAATATGGTGGAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAGAACTCAGAAATC 602
Db 181 TGCATAATATGGTGGAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAGAACTCAGAAATC 240

QY 603 GAGTCTGTGGGAGACACCTCGAGGACAGAACATGTTGGATGGTGGAGCAATAGAACCCAGTTCTA 722
Db 241 GAGTCTGTGGGAGACACCTCGAGGACAGAACATGTTGGATGGTGGAGCAATAGAACCCAGTTCTA 300

QY 663 GACTTACAGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTCTA 722
Db 301 GACTTACAGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTCTA 360

QY 723 CGAGCTGCTGATCAAGAGCTTGGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGCAT 782
Db 361 CGAGCTGCTGATCAAGAGCTTGGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGCAT 420

QY 783 GGATGATTGG 792
Db 421 GGATGATTGG 430

Search completed: July 27, 2005, 09:01:51
Job time : 234 secs
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390 TGTGAGTGTCTCTCAAAATTTGGAGAGTGGTGGAGATCCGATGATCCCGCTGAATC 449  
446 TCCTGGCTGACTTCTGCTGGTGGCTTATGTTGTCATCTGGGCAATTAATGCTCTTT 505  
450 TCCTGGCTGACTTCTGCTGGTGGCTTATGTTGTCATCTGGGCAATTAATGCTCTTT 509  
506 TTGACCGCACACGCACTGCAAGGTCAGTCAATGATGCAAAATATGTTGGAGGAACAG 565  
510 TTGACCGCACACGCACTGCAAGGTCAGTCAATGATGCAAAATATGTTGGAGGAACAG 569  
566 CATATTTAAGTCTCTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAACACCTCGAG 625  
570 CATATTTAAGTCTCTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAACACCTCGAG 629  
626 GACAGAACATGTTGGATGGTGAGACCTTTCTATACGACTTTACAGGACAGCAGATGGGG 685  
630 GACAGAACATGTTGGATGGTGAGACCTTTCTATACGACTTTACAGGACAGCAGATGGGG 689  
686 AATTCATGGCTGTTGAGCAATAGAACCCCGAGTTCTACGAGTGTGATCAAAAGACTTG 745  
690 AATTCATGGCTGTTGAGCAATAGAACCCCGAGTTCTACGAGTGTGATCAAAAGACTTG 749  
746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 805  
750 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 809  
806 AGAAGTTTGCAGATGATTTTGCAGAAAGAGACGAGGAGTGGTGTCAAAATCTTTGACG 865  
810 AGAAGTTTGCAGATGATTTTGCAGAAAGAGACGAGGAGTGGTGTCAAAATCTTTGACG 869  
866 GCACAGATGCTGTGTGATCTCGGTTCTGACTTTTGGAGAGTGTTCATCATGATCACA 925  
870 GCACAGATGCTGTGTGATCTCGGTTCTGACTTTTGGAGAGTGTTCATCATGATCACA 929  
926 ACAGGAGCGGGCTCGTTTATCACAGTGGAGGACGAGCGTGAGCCCCCGCCCTGCAC 985  
930 ACAGGAGCGGGCTCGTTTATCACAGTGGAGGACGAGCGTGAGCCCCCGCCCTGCAC 989  
986 CTCTGCTGTAAACACCCCGACCATCTCTTTCAAAAGGATCCTTTTCATAGAGAAC 1045  
990 CTCTGCTGTAAACACCCCGACCATCTCTTTCAAAAGGATCCTTTTCATAGAGAAC 1049  
1046 ACATGAGAGATCTTGAAGATTTGATTCAGCCGCAAGAGATTTATCAGCTTAAT 1105  
1050 ACATGAGAGATCTTGAAGATTTGATTCAGCCGCAAGAGATTTATCAGCTTAAT 1109  
1106 CAGATAAATCAATCAAAATTAAGTAAAGCTAGTCTC 1146  
1110 CAGATAAATCAATCAAAATTAAGTAAAGCTAGTCTC 1150

## RESULT 3

US-09-439-313-107

; Sequence 107, Application US/09439313  
; Patent No. 6329505

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqul  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-439-313-107

Query Match 93.4%; Score 1070; DB 3; Length 1621;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCGGGCTGCGCCCGGGCCCGTTCCTGTGCTATGCTCTGTGCTGACTTCGGGG 85  
Db 30 TGGAGCTGTCGGGCTGCGCCCGGGCCCGTTCCTGTGCTATGCTCTGTGCTGACTTCGGGG 89  
QY 86 CGCGTGTGGTACGGTGGAGCCGCGCCCGCTCCCGTACGAGCTGAGCGCTTGGGCCCGGG 145  
Db 90 CGCGTGTGGTACGGTGGAGCCGCGCCCGCTCCCGTACGAGCTGAGCGCTTGGGCCCGGG 149  
QY 146 GCAAGCGCTCGCTAGTGTCTGACCTGAAAGCAGCCGCGGGAGCCGCGCTGTGCGGCGTC 205  
Db 150 GCAAGCGCTCGCTAGTGTCTGACCTGAAAGCAGCCGCGGGAGCCGCGCTGTGCGGCGTC 209  
QY 206 TGTGAAAGCGCTCGGATGTGCTGTGAGCCCTTCCGCGCGGTGTCTATGAGAAACTCC 265  
Db 210 TGTGAAAGCGCTCGGATGTGCTGTGAGCCCTTCCGCGCGGTGTCTATGAGAAACTCC 269  
QY 266 AGCTGGGCCCCAGAGTCTGAGCGGGGAAATCCAAAGCTTATTTATGCCAGGCTGAGTG 325  
Db 270 AGCTGGGCCCCAGAGTCTGAGCGGGGAAATCCAAAGCTTATTTATGCCAGGCTGAGTG 329  
QY 326 GATTGGCCAGTCAGGAAAGCTTCTGCGCGTTAGCTGGCCAGCATATCAACTATTTTGGCTT 385  
Db 330 GATTGGCCAGTCAGGAAAGCTTCTGCGCGTTAGCTGGCCAGCATATCAACTATTTTGGCTT 389  
QY 386 TGTGAGTGTCTCTCAAAATTTGGCAAGTGTGAGAAATCCGATGCCCGCTGAATC 445  
Db 390 TGTGAGTGTCTCTCAAAATTTGGCAAGTGTGAGAAATCCGATGCCCGCTGAATC 449  
QY 446 TCCTGGCTGACTTGTGCTGGTGGCTTATGTTGCACTGGGCATTTATATGCTCTTT 505  
Db 450 TCCTGGCTGACTTGTGCTGGTGGCTTATGTTGCACTGGGCATTTATATGCTCTTT 509  
QY 506 TTGACCGCACACGCACTGGCAAGGCTCAGGTCATTGATGCAAAATATGTTGGAAGAACAG 565  
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QY 566 CATATTTAAGTCTTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAACACCTCGAG 625  
Db 570 CATATTTAAGTCTTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAACACCTCGAG 629  
QY 626 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 685  
Db 630 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 689  
QY 686 AATTTCATGGCTGTTGGAGCAATAGAACCCCGAGTTCTACGAGTGTGATCAAAAGACTTG 745  
Db 690 AATTTCATGGCTGTTGGAGCAATAGAACCCCGAGTTCTACGAGTGTGATCAAAAGACTTG 749  
QY 746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 805  
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QY 806 AGAAGTTTGCAGATGATTTTGCAGAAAGAGCAGGAGTGGTGTCAAAATCTTTGACG 865  
Db 810 AGAAGTTTGCAGATGATTTTGCAGAAAGAGCAGGAGTGGTGTCAAAATCTTTGACG 869  
QY 866 GCACAGATGCTGTGTGACTCCCGTTCCTGACTTTTGGAGAGTGTTCATCATGATCACA 925  
Db 870 GCACAGATGCTGTGTGACTCCCGTTCCTGACTTTTGGAGAGTGTTCATCATGATCACA 929  
QY 926 ACAAGGAACGGGGCTCGTTTATCACAGTGGAGGACGAGCGTGAGCCCCCGCCCTGCAC 985



Db 30 TGGAGCTGTCCGGCTTGGCCCGGCGGCTTCTGTGCTATGCTCTGGCTGACTTCGGGG 89  
Qy 86 CGCGTGTGGTACGGCTGAGACCGGCGGCTCCCGCTACGACGTGAGCGCTTTGGCCCGGG 145  
Db 90 CGCGTGTGGTACGGCTGAGACCGGCGGCTCCCGCTACGACGTGAGCGCTTTGGCCCGGG 149  
Qy 146 GCAAGCGCTCGCTAGTGTGACCTGGAAGCAGCAGCGCGGGAGCGCCGCTGCTGGCGGTC 205  
Db 150 GCAAGCGCTCGCTAGTGTGACCTGGAAGCAGCAGCGCGGGAGCGCCGCTGCTGGCGGTC 209  
Qy 206 TGTGCAAGCGGTGCGATGCTGTCTGGAGCCCTTCCGCGCGGTGTCAATGAGAAACTCC 265  
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Qy 266 AGCTGGGCCAGAGATTCGACGCGGGAATAATCCAAAGCTTATTTATGCCAGGCTGAGTG 325  
Db 270 AGCTGGGCCAGAGATTCGACGCGGGAATAATCCAAAGCTTATTTATGCCAGGCTGAGTG 329  
Qy 326 GATTTGGCCAGTCAGGAAGCTTTCGCGGTAGCTGGCCAGCATCAACTATTTGGCTT 385  
Db 330 GATTTGGCCAGTCAGGAAGCTTTCGCGGTAGCTGGCCAGCATCAACTATTTGGCTT 389  
Qy 386 TGTGAGGTGTTCTCTCAAAAATGSCAGAGTGTGAGAATCCGCTATGCCCGCTGAATC 445  
Db 390 TGTGAGGTGTTCTCTCAAAAATGSCAGAGTGTGAGAATCCGCTATGCCCGCTGAATC 449  
Qy 446 TCCTGGCTGACTTGTGCTGGTGGCTTATGTGTGACCTGGGCAATTAATATGGCTCTTT 505  
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Qy 506 TTGACCGCACACGCACTGGCAAGGCTCAGGTCAATGATGCAAAATATGTGGAAGAAACAG 565  
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Qy 566 CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGAAACACTCGAG 625  
Db 570 CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGAAACACTCGAG 629  
Qy 626 GACGAAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 685  
Db 630 GACGAAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 689  
Qy 686 AATTCATGGCTGTTGGAGCAATFAGAAACCCAGTTCACGAGTGTGATCAAAAGGACTTG 745  
Db 690 AATTCATGGCTGTTGGAGCAATFAGAAACCCAGTTCACGAGTGTGATCAAAAGGACTTG 749  
Qy 746 GACTAAAGTCTGATGAACCTTCCCATCAGATGAGCATGGATGATGGCCAGAAATGAAGA 805  
Db 750 GACTAAAGTCTGATGAACCTTCCCATCAGATGAGCATGGATGATGGCCAGAAATGAAGA 809  
Qy 806 AGAAGTTTGCAGATGTAATTTGCAAGAAGACGAGGAGAGTGGTGTCAAAATCTTTGACG 865  
Db 810 AGAAGTTTGCAGATGTAATTTGCAAGAAGACGAGGAGAGTGGTGTCAAAATCTTTGACG 869  
Qy 866 GCACAGATGCTGTGTGACTCCGCTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 925  
Db 870 GCACAGATGCTGTGTGACTCCGCTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 929  
Qy 926 ACAAGGAACGGGGCTCGTTTATACCATGAGGAGCAGGATGAGCCCCCGCTGAC 985  
Db 930 ACAAGGAACGGGGCTCGTTTATACCATGAGGAGCAGGATGAGCCCCCGCTGAC 989  
Qy 986 CTCTGCTGTAAACACCCAGCCATCCCTTCTTTCAAAAGGATCTTTTCATAGAGAAC 1045  
Db 990 CTCTGCTGTAAACACCCAGCCATCCCTTCTTTCAAAAGGATCTTTTCATAGAGAAC 1049  
Qy 1046 ACACGTGAGAGATCTTGAAGAAATTTGATTCAGCCGGAAGAGATTTATCAGCTTAACT 1105  
Db 1050 ACACGTGAGAGATCTTGAAGAAATTTGATTCAGCCGGAAGAGATTTATCAGCTTAACT 1109  
Qy 1106 CAGATAAAATCATTTGAAGTAATTAAGTTAAAGCTAGTCTC 1146

Db 1110 CAGATAAAATCATTTGAAGTAATTAAGTTAAAGCTAGTCTC 1150  
RESULT 6  
US-09-159-812-107  
; Sequence 107, Application US/09159812A  
; Patent No. 6613872  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF  
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.428C5  
; CURRENT APPLICATION NUMBER: US/09/159,812A  
; CURRENT FILING DATE: 1998-09-23  
; NUMBER OF SEQ ID NOS: 306  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-159-812-107  
Query Match 93.4%; Score 1070; DB 4; Length 1621;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 26 TGGAGCTGTCCGGCTTGGCCCGGCGGCTTCTGTGCTATGCTCTGGCTGACTTCGGGG 85  
Db 30 TGGAGCTGTCCGGCTTGGCCCGGCGGCTTCTGTGCTATGCTCTGGCTGACTTCGGGG 89  
Qy 86 CGCGTGTGGTACGGCTGGAACCGGCGGCTCCCGCTACGACGTGAGCGCTTTGGCCCGGG 145  
Db 90 CGCGTGTGGTACGGCTGGAACCGGCGGCTCCCGCTACGACGTGAGCGCTTTGGCCCGGG 149  
Qy 146 GCAAGCGCTCGCTAGTGTGACCTGGAAGCAGCAGCGCGGGAGCGCCGCTGCTGGCGGTC 205  
Db 150 GCAAGCGCTCGCTAGTGTGACCTGGAAGCAGCAGCGCGGGAGCGCCGCTGCTGGCGGTC 209  
Qy 206 TGTGCAAGCGGTGCGATGCTGTCTGGAGCCCTTCCGCGCGGTGTCAATGAGAAACTCC 265  
Db 210 TGTGCAAGCGGTGCGATGCTGTCTGGAGCCCTTCCGCGCGGTGTCAATGAGAAACTCC 269  
Qy 266 AGCTGGGCCAGAGATTCGACGCGGGAATAATCCAAAGCTTATTTATGCCAGGCTGAGTG 325  
Db 270 AGCTGGGCCAGAGATTCGACGCGGGAATAATCCAAAGCTTATTTATGCCAGGCTGAGTG 329  
Qy 326 GATTTGGCCAGTCAGGAAGCTTTCGCGGTAGCTGGCCAGCATCAACTATTTGGCTT 385  
Db 330 GATTTGGCCAGTCAGGAAGCTTTCGCGGTAGCTGGCCAGCATCAACTATTTGGCTT 389  
Qy 386 TGTGAGGTGTTCTCTCAAAAATGSCAGAGTGTGAGAATCCGCTATGCCCGCTGAATC 445  
Db 390 TGTGAGGTGTTCTCTCAAAAATGSCAGAGTGTGAGAATCCGCTATGCCCGCTGAATC 449  
Qy 446 TCCTGGCTGACTTGTGCTGGTGGCTTATGTGTGACCTGGGCAATTAATATGGCTCTTT 505  
Db 450 TCCTGGCTGACTTGTGCTGGTGGCTTATGTGTGACCTGGGCAATTAATATGGCTCTTT 509  
Qy 506 TTGACCGCACACGCACTGGCAAGGCTCAGGTCAATGATGCAAAATATGTGGAAGAAACAG 565  
Db 510 TTGACCGCACACGCACTGGCAAGGCTCAGGTCAATGATGCAAAATATGTGGAAGAAACAG 569  
Qy 566 CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGAAACACTCGAG 625  
Db 570 CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGAAACACTCGAG 629  
Qy 626 GACGAAACATGTTGGATGGTGAGCACCTTTCTATAGACTTACAGGACAGCATGGGG 685  
Db 630 GACGAAACATGTTGGATGGTGAGCACCTTTCTATAGACTTACAGGACAGCATGGGG 689  
Qy 686 AATTCATGGCTGTTGGAGCAATFAGAAACCCAGTTCACGAGTGTGATCAAAAGGACTTG 745







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Db 150 GCAAGCGCTCGCTAGTGTGTGACCTGGAAGACCGCGGGGAGCCCGTGTGCTGGCGGTC 209
Qy 206 TGTGCAAGCGCTCGGATGCTGTGCTGGAGCCCTTCCCGCGGGGTGTATGAGAGAACTCC 265
Db 210 TGTGCAAGCGCTCGGATGCTGTGCTGGAGCCCTTCCCGCGGGGTGTATGAGAGAACTCC 269
Qy 266 AGCTGGGCCCCAGAGATTCGACAGCGGGGAAATCAAAGGCTTATTATGCCAGGCTGAGTG 325
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Qy 326 GATTGGCGCAGTCAGGAAGCTTTCGCGGTGTAGCTGGCCACGATATCAACTATTATTGGCTT 385
Db 330 GATTGGCGCAGTCAGGAAGCTTTCGCGGTGTAGCTGGCCACGATATCAACTATTATTGGCTT 389
Qy 386 TGTGAGGTGTCTCTCAAAATTTGGCAGAGTGGTGAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTCTCTCAAAATTTGGCAGAGTGGTGAATCCGTATGCCCGCTGAATC 449
Qy 446 TCCTGGCTGACTTTCGCTGGTGGCCCTTATGTGTGCACTGGCAATTATAATGCTCTTT 505
Db 450 TCCTGGCTGACTTTCGCTGGTGGCCCTTATGTGTGCACTGGCAATTATAATGCTCTTT 509
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Db 510 TTGACCGCACACGCACTGACAAGGTCAGGTCAATTGATGAAATATGTTGGAGAAACAG 569
Qy 566 CATATTTAAGTTCCTTCTGTTGGAATCTCAGAACTCGAGTCTGTGGAGCACTCGAG 625
Db 570 CATATTTAAGTTCCTTCTGTTGGAATCTCAGAACTCGAGTCTGTGGAGCACTCGAG 629
Qy 626 GACAGAACATGTGTGATGGTGAGCACCTTTCTATACGACTTACAGGACAGACATGGG 685
Db 630 GACAGAACATGTGTGATGGTGAGCACCTTTCTATACGACTTACAGGACAGACATGGG 689
Qy 745 AATTATGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 749
Db 749 AATTATGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 749
Qy 746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGGATGTTGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGGATGTTGGCCAGAAATGAAGA 809
Qy 806 AGAAGTTTGCAGATGTATTTGCAAGAGACGAAAGGACAGTGGTGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGTATTTGCAAGAGACGAAAGGACAGTGGTGTCAAAATCTTTGACG 869
Qy 925 GCACAGATGCTGTGTGACTCCGTTCTGAATTTTGGAGAGGTTGTTATCATGATCACA 929
Db 929 GCACAGATGCTGTGTGACTCCGTTCTGAATTTTGGAGAGGTTGTTATCATGATCACA 929
Qy 926 ACAAGGAACGGGCTCGTTTATCACCAGTGAAGGACAGGACGTGAGCCCCCGCTGCAC 985
Db 930 ACAAGGAACGGGCTCGTTTATCACCAGTGAAGGACAGGACGTGAGCCCCCGCTGCAC 989
Qy 986 CTCTGCTGTAAACACCCCGACCTCTTTTCAAAAGGATCTTTTATAGAGAAC 1045
Db 990 CTCTGCTGTAAACACCCCGACCTCTTTTCAAAAGGATCTTTTATAGAGAAC 1049
Qy 1046 ACATGAGGAGATCTTGAAGAAATTTGATTCAGCCGGAAGAGATTTATCAGCTTAACT 1105
Db 1050 ACATGAGGAGATCTTGAAGAAATTTGATTCAGCCGGAAGAGATTTATCAGCTTAACT 1109
Qy 1106 CAGATAAATCATTTGAAGTAAATAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAATCATTTGAAGTAAATAGGTAAAGCTAGTCTC 1150
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RESULT 10

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US-09-688-489-107
; Sequence 107, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FaetSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-107
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Query Match 93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 TGGAGCTGTCCGGCTGGCCCGGCGCCCGTTCGTGTATGGTCTCTGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCTGGCCCGGCGCCCGTTCGTGTATGGTCTCTGGCTGACTTCGGGG 89
Qy 86 CGGTGTGTGTAACGGTGGACCGGCTCCCGTACGAGCTGAGCGCTTGGCCGGG 145
Db 90 CGGTGTGTGTAACGGTGGACCGGCTCCCGTACGAGCTGAGCGCTTGGCCGGG 149
Qy 146 GCAAGCGCTCGCTAGTGTGCTGAGCCTGAAGCAGCCCGGGAGCCCGTGTGGCGGTC 205
Db 150 GCAAGCGCTCGCTAGTGTGCTGAGCCTGAAGCAGCCCGGGAGCCCGTGTGGCGGTC 209
Qy 206 TGTCAAGCGCTCGGATGTCTGCTGAGCGCTTCCCGCGGGTGTATGAGAGAACTCC 265
Db 210 TGTCAAGCGCTCGGATGTCTGCTGAGCGCTTCCCGCGGGTGTATGAGAGAACTCC 269
Qy 266 AGCTGGGCCAGAGATTCGACGCGGAAATCAAAGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCAGAGATTCGACGCGGAAATCAAAGCTTATTTATGCCAGGCTGAGTG 329
Qy 326 GATTGGCCAGTCAGGAAGCTTTCGCGGTGTAGCTGGCCAGCATCAACTATTGGCTT 385
Db 330 GATTGGCCAGTCAGGAAGCTTTCGCGGTGTAGCTGGCCAGCATCAACTATTGGCTT 389
Qy 386 TGTGAGGTGTCTCTCAAAATTTGGCAGAGTGGTGAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTCTCTCAAAATTTGGCAGAGTGGTGAATCCGTATGCCCGCTGAATC 449
Qy 446 TCCTGGCTGACTTTCGCTGGTGGCCCTTATGTGTGCACTGGGCAATTATAATGCTCTTT 505
Db 450 TCCTGGCTGACTTTCGCTGGTGGCCCTTATGTGTGCACTGGGCAATTATAATGCTCTTT 509
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Db 510 TTGACCGCACACGCACTGACAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGAAACAG 569
Qy 566 CATATTTAAGTTCCTTCTGTTGGAATCTCAGAACTCGAGTCTGTGGAGCACTCGAG 625
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Qy 626 GACAGAACATGTGTGATGGTGAGCACCTTTCTATACGACTTACAGGACAGACATGGG 685
Db 630 GACAGAACATGTGTGATGGTGAGCACCTTTCTATACGACTTACAGGACAGACATGGG 689
Qy 686 AATTATGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 745
Db 690 AATTATGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 749
Qy 746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGGATGTTGGCCAGAAATGAAGA 805
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Db      750 GACTAAAGTCTGATGAACTTCCCATCAGATGAGCATGGATGATTTGGCCAGAAATGAAGA 809
QY      806 AGAAGTTGACAGATGATTTGCAAGAGAGACGAGGAGTGTCAAATCTTTTGACG 865
Db      810 AGAAGTTGACAGATGATTTGCAAGAGAGACGAGGAGTGTCAAATCTTTTGACG 869
QY      866 GCACAGATGCCGTGCTGAGTCCGGTCTGACATTTTGGAGAGTGTTCATCATGATCACA 925
Db      870 GCACAGATGCCGTGCTGAGTCCGGTCTGACATTTTGGAGAGTGTTCATCATGATCACA 929
QY      926 ACAAGGAACGGGGCTCGTTTATCACAGTACAGAGCAGAGCATGAGCCCGCCCTGCAC 985
Db      930 ACAAGGAACGGGGCTCGTTTATCACAGTACAGAGCAGAGCATGAGCCCGCCCTGCAC 989
QY      986 CTCTGCTGTAAACACCCAGCCATCCCTTTTCAAAGGGATCCTTTTCATAGGAGAAC 1045
Db      990 CTCTGCTGTAAACACCCAGCCATCCCTTTTCAAAGGGATCCTTTTCATAGGAGAAC 1049
QY      1046 ACACGTAGGAGATCTTGAAGATTTGGATTGAGCCGCGAGAGATTTTATCAGCTTAACT 1105
Db      1050 ACACGTAGGAGATCTTGAAGATTTGGATTGAGCCGCGAGAGATTTTATCAGCTTAACT 1109
QY      1106 CAGATAAAATCAATGAAAGTAAAGGTAAAGCTAGTCTC 1146
Db      1110 CAGATAAAATCAATGAAAGTAAAGGTAAAGCTAGTCTC 1150

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RESULT 11

US-09-679-426-107.  
; Sequence 107, Application US/09679426  
; Patent No. 6759515

GENERAL INFORMATION:

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

```

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C20

CURRENT FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 895

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 107

LENGTH: 1621

TYPE: DNA

ORGANISM: Homo sapien

US-09-679-426-107

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Query Match      93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      26 TGGAGCTGTCCGGCTGCGCCCGCCCGTCTGTGCTATGCTCTGCTGACATTCGGGG 85
Db      30 TGGAGCTGTCCGGCTGCGCCCGCCCGTCTGTGCTATGCTCTGCTGACATTCGGGG 89
QY      86 CCGTGTGTGATGAGTGGACCGCCCGCTCCCGCTACGATGAGCGCTTGGCCCGGG 145

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RESULT 12

US-09-759-143-107

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QY      206 TGTGCAAGCGCTCGAGTGTGCTGTGGAGCCCTTCCGCGCGGCTGTGATGAGAACTCC 265
Db      210 TGTGCAAGCGCTCGAGTGTGCTGTGGAGCCCTTCCGCGCGGCTGTGATGAGAACTCC 269
QY      266 AGCTGGGCCCCAGAGATTCGACAGCGGGAATAATCCAAGCTTATTTATGCCAGGCTGAGTG 325
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Db      450 TCCTGGCTGACTTTGTGCTGCTGCTTATGTGTGCACTGGGCATTAATATGGCTCTTT 509
QY      506 TTGACCCGACACGCACTGGCAAGGTTCAGGTCAATTGATGCAAAATATGTTGGAGGAACAG 565
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QY      566 CATATTTAAGTCTTTCTGTGGAAATCTCAGAAATCGAGTCTGTGGAGACGACCTCGAG 625
Db      570 CATATTTAAGTCTTTCTGTGGAAATCTCAGAAATCGAGTCTGTGGAGACGACCTCGAG 629
QY      626 GACAGACATCTTGGATGGTGGACCATCTTCTATACGACTTACAGGACAGCAGATGGG 685
Db      630 GACAGACATCTTGGATGGTGGACCATCTTCTATACGACTTACAGGACAGCAGATGGG 689
QY      686 AATTGATGGCTTGTGGAGCAATAGAACCCCGAGTTCTACGAGCTGTGATCAAGGACTTG 745
Db      690 AATTGATGGCTTGTGGAGCAATAGAACCCCGAGTTCTACGAGCTGTGATCAAGGACTTG 749
QY      746 GACTTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGGATGTTGGCCAGAAATGAAGA 805
Db      750 GACTTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGGATGTTGGCCAGAAATGAAGA 809
QY      806 AGAAGTTTGCAGATGTATTTGCAAGAGAGCAAGGAGAGTGGTGTCAAATCTTTTGACG 865
Db      810 AGAAGTTTGCAGATGTATTTGCAAGAGAGCAAGGAGAGTGGTGTCAAATCTTTTGACG 869
QY      866 GCACAGATGCTGTGATCTCCGGTCTCTGACTTTTGGAGAGTGTGTTTATCATGATCACA 925
Db      870 GCACAGATGCTGTGATCTCCGGTCTCTGACTTTTGGAGAGTGTGTTTATCATGATCACA 929
QY      926 ACAAGGAACGGGGCTCGTTTATCACAGTACAGGAGCAGAGCTGAGCCCGCCCTGCAC 985
Db      930 ACAAGGAACGGGGCTCGTTTATCACAGTACAGGAGCAGAGCTGAGCCCGCCCTGCAC 989
QY      986 CTCTGCTGTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTTCATAGGAGAAC 1045
Db      990 CTCTGCTGTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTTCATAGGAGAAC 1049
QY      1046 ACACGTAGGAGATCTTGAAGATTTGGATTGAGCCGCGAGAGATTTTATCAGCTTAACT 1105
Db      1050 ACACGTAGGAGATCTTGAAGATTTGGATTGAGCCGCGAGAGATTTTATCAGCTTAACT 1109
QY      1106 CAGATAAAATCAATGAAAGTAAAGGTAAAGCTAGTCTC 1146
Db      1110 CAGATAAAATCAATGAAAGTAAAGGTAAAGCTAGTCTC 1150

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Db 247 GCCTGTGTGACTCGGTTCTGACTTTTGAGAGAGTTGTTTCATCATGATCACAACAGGAA 306  
Qy 934 CGGGGCTCGTTTATCACCAGTGAGGACAGACAGTGTAGCCCCGCCCTGACCTCTGCTG 993  
Db 307 CGGGGCTCGTTTATCACCAGTGAGGACAGACAGTGTAGCCCCGCCCTGACCTCTGCTG 366  
Qy 994 TTAACACCCAGCATCCCTCTTTCAAAAGGGATCC 1031  
Db 367 TTAACACCCAGCATCCCTCTTTCAAAAGGGATCC 404

## RESULT 15

US-09-030-607-2  
; Sequence 2, Application US/09030607  
; Patent No. 6262245  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,607  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Makl, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 816 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-030-607-2

Query Match 34.7%; Score 398; DB 3; Length 816;  
Best Local Similarity 100.0%; Pred. No. 7.3e-195;  
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 7 ATGTTGGATGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGGAATTCATG 66  
Qy 694 GCTGTTGGAGCAATAGACCCCGTCTTACGAGCTGCTGATCAAGGACTTGGACTAAAG 753  
Db 67 GCTGTTGGAGCAATAGACCCCGTCTTACGAGCTGCTGATCAAGGACTTGGACTAAAG 126  
Qy 754 TCTGATGAACCTCCCAATCAGATGAGCATGATGATGGCCAGAGAAATGAAGAAGATT 813  
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Qy 814 GCAGATGTATTGCAAGAACGACGAGTGTGTCAAAATCTTTTGACGGCACAGAT 873  
Db 187 GCAGATGTATTGCAAGAACGACGAGTGTGTCAAAATCTTTTGACGGCACAGAT 246

Qy 874 GCCTGTGTGACTCGGTTCTGACTTTTGAGAGAGTTTTCATCATGATCACAACAGGAA 933  
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Qy 934 CGGGGCTCGTTTATCACCAGTGAGGACAGACAGTGTAGCCCCGCCCTGACCTCTGCTG 993  
Db 307 CGGGGCTCGTTTATCACCAGTGAGGACAGACAGTGTAGCCCCGCCCTGACCTCTGCTG 366  
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Db 367 TTAACACACCCAGCATCCCTCTTTCAAAAGGGATCC 404

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GenCore version 5.1.6  
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12: geneseqn2004as.\*  
13: geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 1146  | 100.0       | 2005   | 6  | AAD38607 Human alp |
| 2          | 1146  | 100.0       | 2005   | 6  | AAD38603 Human alp |
| 3          | 1146  | 100.0       | 2005   | 10 | Add18532 Human pro |
| 4          | 1146  | 100.0       | 2040   | 13 | Acn38207 Tumour-as |
| 5          | 1146  | 100.0       | 2069   | 6  | AAD38604 Human alp |
| 6          | 1146  | 100.0       | 2069   | 10 | Adb75193 Prostate  |
| 7          | 1132  | 98.8        | 3654   | 6  | AAD38605 Human alp |
| 8          | 1132  | 98.8        | 3654   | 10 | Adb75195 Prostate  |
| 9          | 1095  | 95.5        | 2069   | 10 | Adb75201 Prostate  |
| 10         | 1081  | 94.3        | 2626   | 10 | Adb75203 Prostate  |
| 11         | 1070  | 93.4        | 1621   | 2  | Aav58584 Prostate  |
| 12         | 1070  | 93.4        | 1621   | 2  | AAV61199 Full leng |
| 13         | 1070  | 93.4        | 1621   | 3  | AAO6347 Human imm  |
| 14         | 1070  | 93.4        | 1621   | 3  | AB971252 Human pro |
| 15         | 1070  | 93.4        | 1621   | 4  | AH93463 Human pro  |
| 16         | 1070  | 93.4        | 1621   | 4  | AA63555 Human pro  |
| 17         | 1070  | 93.4        | 1621   | 4  | AAH02528 Prostate  |
| 18         | 1070  | 93.4        | 1621   | 4  | AH84777 Human pro  |
| 19         | 1070  | 93.4        | 1621   | 5  | ACA59364 Prostate  |
| 20         | 1070  | 93.4        | 1621   | 5  | AAS10106 Human pro |

|    |      |      |      |    |                    |
|----|------|------|------|----|--------------------|
| 21 | 1070 | 93.4 | 1621 | 6  | ABL94927 Human Fl- |
| 22 | 1070 | 93.4 | 1621 | 6  | AB58636 Prostate   |
| 23 | 1070 | 93.4 | 1621 | 8  | ACC95091 Prostate  |
| 24 | 1070 | 93.4 | 1621 | 10 | ADB13557 Human pro |
| 25 | 1070 | 93.4 | 1621 | 10 | ADG26973 Human pro |
| 26 | 1070 | 93.4 | 2376 | 5  | ABV25239 Human pro |
| 27 | 1070 | 93.4 | 2376 | 5  | ABV21293 Human pro |
| 28 | 1070 | 93.4 | 2376 | 5  | ABV21881 Human pro |
| 29 | 1070 | 93.4 | 2376 | 5  | ABV27112 Human pro |
| 30 | 1019 | 88.9 | 1674 | 4  | AAH13696 Human cDN |
| 31 | 797  | 69.5 | 1294 | 5  | ABV22733 Human pro |
| 32 | 797  | 69.5 | 1294 | 5  | ABV28442 Human pro |
| 33 | 797  | 69.5 | 1294 | 5  | ABV28544 Human pro |
| 34 | 797  | 69.5 | 1294 | 5  | ABV22620 Human pro |
| 35 | 797  | 69.5 | 1294 | 5  | ABV27711 Human pro |
| 36 | 756  | 66.0 | 1039 | 4  | AAC91303 Human pol |
| 37 | 740  | 64.6 | 1316 | 10 | ADB75199 Prostate  |
| 38 | 613  | 53.5 | 1317 | 4  | AAH17637 Human cDN |
| 39 | 595  | 51.9 | 2946 | 10 | ADB75205 Prostate  |
| 40 | 595  | 51.9 | 2946 | 12 | ADP56742 Human alp |
| 41 | 595  | 51.9 | 3023 | 6  | AAD38606 Human alp |
| 42 | 595  | 51.9 | 3023 | 10 | ADB75197 Prostate  |
| 43 | 524  | 45.7 | 720  | 4  | AAH03341 Human cDN |
| 44 | 498  | 43.5 | 729  | 12 | ADP56741 Human alp |
| 45 | 493  | 43.0 | 865  | 5  | ABV28560 Human pro |

## ALIGNMENTS

RESULT 1  
AAD38607  
ID AAD38607 standard; cDNA; 2005 BP.  
XX  
AC AAD38607;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human alpha-methylacyl-CoA racemase splice variant, SV4 cDNA.  
XX  
KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;  
KW cytosolic; SV4; gene; ss.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
CDS 66..1214  
FT /\*tag= a  
FT /product= "Human SV4 protein"  
XX  
FN WO200227324-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 28-SEP-2001; 2001WO-US030532.  
XX  
PR 28-SEP-2000; 2000US-0236238P.  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Richardson J, Monahan J;  
DR WPI; 2002-405070/43.  
DR P-PSDB; AAE23975.  
XX  
PT Determining risk for prostate cancer in subject or risk for metastatic  
PT prostate cancer to liver or lymph nodes of prostate cancer patients,  
PT comprises measuring expression or activity of alpha-methylacyl-CoA  
PS Claim 54; Fig 9; 102pp; English.  
CC The present invention relates to novel methods for determining whether an

CC individual is at risk for prostate cancer or whether a prostate cancer  
CC patient is at risk for metastatic prostate cancer to the liver or lymph  
CC nodes. The method involves measuring the expression or activity of alpha-  
CC methylacyl-CoA racemase. Sequences of the invention are useful in  
CC diagnostic methods, drug screening assays, and in treating or preventing  
CC cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-  
CC acyl-CoA racemase splice variant, SV4 cDNA  
XX  
SQ Sequence 2005 BP; 520 A; 427 C; 514 G; 544 T; 0 U; 0 Other;

Query Match 100.0%; Score 1146; DB 6; Length 2005;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCACTGACGGGATCTCGGTGCTGGAGCTGTCCGGCCTGGCCCGGGCCCTTCTGT 60  
Db 66 ATGGCACTGACGGGATCTCGGTGCTGGAGCTGTCCGGCCTGGCCCGGGCCCTTCTGT 125

Qy 61 GCTATGGTCTCGGTGACTTCGGGGCGGTGTGGTACGCGTGGACCGGCCCGGTCCCGC 120  
Db 126 GCTATGGTCTCGGTGACTTCGGGGCGGTGTGGTACGCGTGGACCGGCCCGGTCCCGC 185

Qy 121 TACGACGTGAGCCGCTTGGCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180  
Db 186 TACGACGTGAGCCGCTTGGCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 245

Qy 181 CGGGAGCGCGGTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240  
Db 246 CGGGAGCGCGGTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 305

Qy 241 CGCGCGGTGTATGAGGAACTCCAGCTGGCGGCCAGAGATCTGCGCGGGAAATCCA 300  
Db 306 CGCGCGGTGTATGAGGAACTCCAGCTGGCGGCCAGAGATCTGCGCGGGAAATCCA 365

Qy 301 AGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360  
Db 366 AGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425

Qy 361 GGCCACGATATCACTATTGGCTTTGTCAAGTGTCTCTCAAAAATGGCAGAGTGT 420  
Db 426 GGCCACGATATCACTATTGGCTTTGTCAAGTGTCTCTCAAAAATGGCAGAGTGT 485

Qy 421 GAGAACTCGTATGCCCGCTGAATCTCTGCTGACTTTGTGTTGGTGGCTTATGTGT 480  
Db 486 GAGAACTCGTATGCCCGCTGAATCTCTGCTGACTTTGTGTTGGTGGCTTATGTGT 545

Qy 481 GCATGGGCATTATATGGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAGGTCAAT 540  
Db 546 GCATGGGCATTATATGGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAGGTCAAT 605

Qy 541 GATGCAATATGGTGAAGGACAGCATATTTAAGTCTTTTCTGTGGAAACTCAGAA 600  
Db 606 GATGCAATATGGTGAAGGACAGCATATTTAAGTCTTTTCTGTGGAAACTCAGAA 665

Qy 601 TCGAGTCTGTGGAGACCTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 660  
Db 666 TCGAGTCTGTGGAGACCTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 725

Qy 661 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720  
Db 726 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 785

Qy 721 TACGAGTCTGTCAAAAGGACTTGGACTTAAGTCTGATGAACCTTCCCAATCAGATGAC 780  
Db 786 TACGAGTCTGTCAAAAGGACTTGGACTTAAGTCTGATGAACCTTCCCAATCAGATGAC 845

Qy 781 ATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAGACGAG 840  
Db 846 ATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAGACGAG 905

Qy 841 CGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGACTTTT 900  
Db 906 CGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGACTTTT 965

Qy 901 GAGGAGTGTCTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960  
Db 966 GAGGAGTGTCTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1025

Qy 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020  
Db 1026 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085

Qy 1021 AAAGGGATCTTTATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1080  
Db 1086 AAAGGGATCTTTATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1145

Qy 1081 CGCGAAGAGATTTATCAGCTTAAGTCAAGATAAATCAATTAAGTAAAGTAAAGCT 1140  
Db 1146 CGCGAAGAGATTTATCAGCTTAAGTCAAGATAAATCAATTAAGTAAAGTAAAGCT 1205

Qy 1141 AGTCTC 1146  
Db 1206 AGTCTC 1211

RESULT 2  
AAD38603  
ID AAD38603 standard; cDNA; 2005 BP.  
XX  
AC AAD38603;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human alpha-methylacyl-CoA racemase SV1 cDNA #1.  
XX  
KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;  
KW cytosolic; SV1; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Location/Qualifiers  
FT CDS  
FT 66..1214  
FT /\*tag= a  
FT /product= "Human SV1 protein #1"  
FT /note= "This region is specifically claimed as SEQ ID NO:  
FT 3 in claim 54 of the specification"  
XX  
PN WO200227324-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 28-SEP-2001; 2001WO-US030532.  
XX  
PR 28-SEP-2000; 2000US-0236238P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Richardson J, Monahan J;  
XX  
DR WPI; 2002-405070/43.  
DR P-PSDB; AAE23971.  
XX  
XX Determining risk for prostate cancer in subject or risk for metastatic  
XX prostate cancer to liver or lymph nodes of prostate cancer patients,  
XX comprises measuring expression or activity of alpha-methylacyl-CoA  
XX racemase.  
XX  
PS Claim 54; Fig 1; 102pp; English.  
XX  
XX The present invention relates to novel methods for determining whether an  
XX individual is at risk for prostate cancer or whether a prostate cancer  
XX patient is at risk for metastatic prostate cancer to the liver or lymph  
XX nodes. The method involves measuring the expression or activity of alpha-  
XX methylacyl-CoA racemase. Sequences of the invention are useful in  
XX diagnostic methods, drug screening assays, and in treating or preventing  
XX cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-

|     |   |  |
|-----|---|--|
| CC  | acyl-CoA racemase SV1 cDNA  |  |
| XX  | Sequence 2005 BP; 519 A; 427 C; 514 G; 545 T; 0 U; 0 Other;             |  |
| QQ  | Query Match 100.0%; Score 1146; DB 6; Length 2005;                      |  |
| SS  | Best Local Similarity 100.0%; Pred. No. 0;                              |  |
| TT  | Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;           |  |
| YY  | 1 ATGGCACTGCGAGGCAATCTCGGTCTGAGAGTCTCGGCTGTCGGCCCGGCGCCCGTTCTGT 60      |  |
| ZZ  | 66 ATGGCACTGCGAGGCAATCTCGGTCTGAGAGTCTCGGCTGTCGGCCCGGCGCCCGTTCTGT 125    |  |
| AAA | 61 GCTATGCTCTGGCTGACTTGGGGCGGTGTGTACGGCTGGAGCCCGGCTCCCGC 120            |  |
| BBB | 126 GCTATGCTCTGGCTGACTTGGGGCGGTGTGTACGGCTGGAGCCCGGCTCCCGC 185           |  |
| CCC | 121 TACGACGTGAGCGCTTGGCGGGCAAGCGCTCGTGTGCTGGAGCTGAAGCAGCGC 180          |  |
| DDD | 186 TACGACGTGAGCGCTTGGCGGGCAAGCGCTCGTGTGCTGGAGCTGAAGCAGCGC 245          |  |
| EEE | 181 CGGGAGCGCGGTGCTCGGCGTCTGTGCAAGCGGTCCGATGTCTGTGGAGCCCTTC 240         |  |
| FFF | 246 CGGGAGCGCGGTGCTCGGCGTCTGTGCAAGCGGTCCGATGTCTGTGGAGCCCTTC 305         |  |
| GGG | 241 CGCGCGGTGCTGAGAGAACTCAGCTGGCGCCAGAGATCTGCAGCGGGAAATCCA 300          |  |
| HHH | 306 CGCGCGGTGCTGAGAGAACTCAGCTGGCGCCAGAGATCTGCAGCGGGAAATCCA 365          |  |
| III | 301 AGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCGGTAGCT 360        |  |
| JJJ | 366 AGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCGGTAGCT 425        |  |
| KKK | 361 GCGCACGATCAACTATTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAGTGGT 420          |  |
| LLL | 426 GCGCACGATCAACTATTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAGTGGT 485          |  |
| MMM | 421 GAGAACTCGTATGCCCGCTGAATCTCTGCTGATCTTTGCTGGTGGTGGTCTATGTGT 480       |  |
| NNN | 486 GAGAACTCGTATGCCCGCTGAATCTCTGCTGATCTTTGCTGGTGGTGGTCTATGTGT 545       |  |
| OOO | 481 GCACCTGGCAATTAATAGCTCTTTTTCACCGCACACGCTGCGCAAGGTCAGGTCAAT 540       |  |
| PPP | 546 GCACCTGGCAATTAATAGCTCTTTTTCACCGCACACGCTGCGCAAGGTCAGGTCAAT 605       |  |
| QQQ | 541 GATGCAAAATATGTTGGAGGAAACAGCATATTTAAGTCTTTTCTGTGAAATCTCAGAAA 600     |  |
| RRR | 606 GATGCAAAATATGTTGGAGGAAACAGCATATTTAAGTCTTTTCTGTGAAATCTCAGAAA 665     |  |
| SSS | 601 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAAATGTTGGATGTGGAGCACTTTCTAT 660       |  |
| TTT | 666 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAAATGTTGGATGTGGAGCACTTTCTAT 725       |  |
| UUU | 661 ACGACTTACAGACAGCAGATGGGAATTCATGGCTGTGGGCAATAGAACCCGCTTC 720         |  |
| VVV | 726 ACGACTTACAGACAGCAGATGGGAATTCATGGCTGTGGGCAATAGAACCCGCTTC 785         |  |
| WWW | 721 TACGAGCTGCTGATCAAAAGCACTTGGAACTGATGAATCTCCCAATCAGATGAGC 780         |  |
| XXX | 786 TACGAGCTGCTGATCAAAAGCACTTGGAACTGATGAATCTCCCAATCAGATGAGC 845         |  |
| YYY | 781 ATGGATGATTTGGCCAGAAATAGAGAAAGTTTGCAGATGATTTTGCAGAAAGACGAG 840       |  |
| ZZZ | 846 ATGGATGATTTGGCCAGAAATAGAGAAAGTTTGCAGATGATTTTGCAGAAAGACGAG 905       |  |
| AAA | 841 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900         |  |
| BBB | 906 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 965         |  |
| CCC | 901 GAGGAGGTTGTTTCATCATGATCAACAAAGAAAGCGGGCTCGTTTATCACCAGTGAGGAG 960    |  |
| DDD | 966 GAGGAGGTTGTTTCATCATGATCAACAAAGAAAGCGGGCTCGTTTATCACCAGTGAGGAG 1025   |  |
| EEE | 961 CAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTGTTTAAACACCCCGCAGCCATCCCTTTTC 1020 |  |

|          |             |   |      |
|----------|-------------|---|------|
| Db       | 1026        | CAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCGAGCATCCCTTCTTTC                 | 1085 |
| Qy       | 1021        | AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC             | 1080 |
| Db       | 1086        | AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC             | 1145 |
| Qy       | 1081        | CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCAATGAAAGTAATAAGGTAAGAGCT             | 1140 |
| Db       | 1146        | CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCAATGAAAGTAATAAGGTAAGAGCT             | 1205 |
| Qy       | 1141        | AGTCCTC 1146  |      |
| Db       | 1206        | AGTCCTC 1211  |      |
| RESULT 3 |             |   |      |
| ADD18532 |             |   |      |
| ID       | ADD18532    | standard; DNA; 2005 BP.   |      |
| XX       | AC          | ADD18532;   |      |
| XX       | AC          |   |      |
| DT       | 15-JAN-2004 | (first entry)   |      |
| XX       |             | Human prostate cancer diagnosis related DNA sequence SeqID104.            |      |
| DE       |             | prostate tissue; cancer diagnostic; cancer marker; prostate cancer; PCA;  |      |
| XX       |             | male cancer-related death; serum biomarker; tissue biomarker; cytostatic; |      |
| KW       |             | gene therapy; prostate biopsy tissue; AMACR;                              |      |
| KW       |             | alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth;     |      |
| KW       |             | human; db.  |      |
| XX       |             |   |      |
| OS       |             | Homo sapiens.   |      |
| XX       |             |   |      |
| XX       |             | WO2003012067-A2.  |      |
| XX       |             |   |      |
| PD       |             | 13-FEB-2003.  |      |
| XX       |             |   |      |
| PF       |             | 02-AUG-2002; 2002WO-US024567.   |      |
| XX       |             |   |      |
| PR       |             | 02-AUG-2001; 2001US-0309581P.   |      |
| PR       |             | 15-NOV-2001; 2001US-0334488P.   |      |
| PR       |             | 01-AUG-2002; 2002US-00210120.   |      |
| XX       |             | (UNMI ) UNIV MICHIGAN.  |      |
| PA       |             | Rubin MA, Chinnaiyan AM, Sreekumar A;                                     |      |
| XX       |             |   |      |
| PI       |             | WPI; 2003-278396/27.  |      |
| XX       |             |   |      |
| DR       |             | Characterizing prostate tissue comprises providing a prostate tissue      |      |
| PT       |             | sample from a subject and detecting the presence or absence of expression |      |
| PT       |             | of hepsin, pim-1 or EZH2.   |      |
| XX       |             |   |      |
| PS       |             | Disclosure; Fig 10; 297pp; English.                                       |      |
| XX       |             |   |      |
| CC       |             | This invention relates to a novel method of characterising prostate       |      |
| CC       |             | tissue in a subject and to compositions and methods for cancer            |      |
| CC       |             | diagnostics, including cancer markers, in particular prostate cancer.     |      |
| CC       |             | Prostate cancer (PCA) is a leading cause of male cancer-related death.    |      |
| CC       |             | Additional serum and tissue biomarkers would aid diagnosis. The invention |      |
| CC       |             | may provide means of producing compounds with a cytostatic activity or    |      |
| CC       |             | allow the development of gene therapy. The methods of the invention       |      |
| CC       |             | useful for characterising prostate tissue in a subject, screening         |      |
| CC       |             | compounds, characterising inconclusive prostate biopsy tissue in a        |      |
| CC       |             | subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase)           |      |
| CC       |             | expression in a bodily fluid, characterising tissue in a subject,         |      |
| CC       |             | diagnosing cancer in a subject and inhibiting the growth of cells. The    |      |
| CC       |             | present sequence is a DNA sequence which is preferably utilised in the    |      |
| CC       |             | method of the invention. Note: Two sequences were allocated Seq ID 104 in |      |
| CC       |             | the specification. The other is given in example 7, page 122 (see         |      |
| CC       |             | ADD18551).  |      |
| XX       |             |   |      |





CC used as hybridisation probes, in chromosome and gene mapping, in  
 CC chromosome identification and in gene therapy. The present sequence  
 CC represents a 1AT nucleic acid of the invention  
 XX Sequence 2040 BP; 524 A; 439 C; 529 G; 548 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 1146; DB 13; Length 2040;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ATGGCACTGACGGGATCTCGGCTGAGCTGTCGGGCTGGCCCGGGCCGGCTTCTGT 60  
 90 ATGGCACTGACGGGATCTCGGCTGAGCTGTCGGGCTGGCCCGGGCCGGCTTCTGT 149  
 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 150 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209  
 121 TAGGAGCTGACGGGCTTGGCCCGGGGCAAGCGCTGCTAGTCTGAGCTGAGCAGCG 180  
 210 TAGGAGCTGACGGGCTTGGCCCGGGGCAAGCGCTGCTAGTCTGAGCTGAGCAGCG 269  
 181 CGGGGAGCGCGCTGCTGCGGCGCTGCTGCAAGCGCTGCTGCTGCTGCTGCTGCTGCT 240  
 270 CGGGGAGCGCGCTGCTGCGGCGCTGCTGCAAGCGCTGCTGCTGCTGCTGCTGCTGCT 329  
 241 CGCCCGGCTGCTCATGAGAACTCCAGCTGGGCCAGAGATTCTGAGCGGGAATCCA 300  
 330 CGCCCGGCTGCTCATGAGAACTCCAGCTGGGCCAGAGATTCTGAGCGGGAATCCA 389  
 301 AGGCTTATTTATGAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCGGTTAGCT 360  
 390 AGGCTTATTTATGAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCGGTTAGCT 449  
 361 GCGCAGCATATCACTATTTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 450 GCGCAGCATATCACTATTTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509  
 421 GAGAACTCGTATGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 510 GAGAACTCGTATGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569  
 481 GCATGCGGCTATTAATGCTCTTTTGGCCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 570 GCATGCGGCTATTAATGCTCTTTTGGCCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 629  
 541 GATGCAATATGCTGGAAGGACAGCATATTTAAGTCTTTTCTGGAAGCTCAGAA 600  
 630 GATGCAATATGCTGGAAGGACAGCATATTTAAGTCTTTTCTGGAAGCTCAGAA 689  
 601 TCGAGTCTGTGGGAGCAGCTCGAGCAGACATGTTGGATGTTGGAGCAGCTTTCTAT 660  
 690 TCGAGTCTGTGGGAGCAGCTCGAGCAGACATGTTGGATGTTGGAGCAGCTTTCTAT 749  
 661 ACGACTTACAGCAGCAGATGGGAAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720  
 750 ACGACTTACAGCAGCAGATGGGAAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 809  
 721 TAGGAGCTGCTCATCAAGGACTTGGACTTAAGTCTGATGACTTCCCAATCAGATGAC 780  
 810 TAGGAGCTGCTCATCAAGGACTTGGACTTAAGTCTGATGACTTCCCAATCAGATGAC 869  
 781 ATGGATGATGGCCAGAAATGAAGAGATTTGAGATGATTTGCAAGAGAGAGAGAG 840  
 870 ATGGATGATGGCCAGAAATGAAGAGATTTGAGATGATTTGCAAGAGAGAGAGAG 929  
 841 CGAGAGTGTGTCATTTGACCGGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 930 CGAGAGTGTGTCATTTGACCGGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989  
 901 GAGGAGTGTGTCATTCATGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
 990 GAGGAGTGTGTCATTCATGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1049

961 CAGGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGGCAATCCCTTCTTTC 1020  
 1050 CAGGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGGCAATCCCTTCTTTC 1109  
 1021 AAAAGGGATCTTTATAGAGGAAACACACTGAGGAGTACTTGAAGATTTGGATTGAGC 1080  
 1110 AAAAGGGATCTTTATAGAGGAAACACACTGAGGAGTACTTGAAGATTTGGATTGAGC 1169  
 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAGAGCT 1140  
 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAGAGCT 1229  
 1141 AGTCTC 1146  
 1230 AGTCTC 1235  
 RESULT 5  
 AAD38604  
 ID AAD38604 standard; cDNA; 2069 BP.  
 XX  
 AC AAD38604;  
 XX  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE Human alpha-methylacyl-CoA racemase SV1 cDNA #2.  
 XX  
 KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;  
 KW cytosolic; SV1; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 90..1238  
 FT /\*tag= a  
 FT /product= "Human SV1 protein #2"  
 XX  
 WO200227324-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 28-SEP-2001; 2001WO-US030532.  
 XX  
 PR 28-SEP-2000; 2000US-0236238P.  
 XX  
 (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Richardson J, Monahan J;  
 XX  
 WPI; 2002-405070/43.  
 P-PSDB; AAE23972.  
 XX  
 Determining risk for prostate cancer in subject or risk for metastatic  
 prostate cancer to liver or lymph nodes of prostate cancer patients,  
 comprises measuring expression or activity of alpha-methylacyl-CoA  
 racemase.  
 XX  
 Claim 54; Fig 3; 102pp; English.  
 XX  
 The present invention relates to novel methods for determining whether an  
 individual is at risk for prostate cancer or whether a prostate cancer  
 patient is at risk for metastatic prostate cancer to the liver or lymph  
 nodes. The method involves measuring the expression or activity of alpha-  
 methylacyl-CoA racemase. Sequences of the invention are useful in  
 diagnostic methods, drug screening assays, and in treating or preventing  
 cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-  
 acyl-CoA racemase SV1 cDNA  
 XX  
 Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1146; DB 6; Length 2069;  
 Best Local Similarity 100.0%; Pred. No. 0;

| Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |      |  |      |
|---|------|--|------|
| Qy  | 1    | ATGGCACTGCAGGGGATCTCGGTGTGTGAGCTGTCCGGCTGTGGCCCGGGCCCGTTCGT    | 60   |
| Db  | 90   | ATGGCACTGCAGGGGATCTCGGTGTGTGAGCTGTCCGGCTGTGGCCCGGGCCCGTTCGT    | 149  |
| Qy  | 61   | GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGACGCGTGGACCGGCCCGCTCCGC      | 120  |
| Db  | 150  | GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGACGCGTGGACCGGCCCGCTCCGC      | 209  |
| Qy  | 121  | TACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCG    | 180  |
| Db  | 210  | TACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCG    | 269  |
| Qy  | 181  | CGGGAGCGCGCTGCTCGGGGCTGTGTGAAGCGGTGCGATGTGCTGTGGAGCCCTTC       | 240  |
| Db  | 270  | CGGGAGCGCGCTGCTCGGGGCTGTGTGAAGCGGTGCGATGTGCTGTGGAGCCCTTC       | 329  |
| Qy  | 241  | CGCCCGGTGTCTGAGGAACTCCAGCTGGGCCCGCAGAGATTCGACGGGGAATCCA        | 300  |
| Db  | 330  | CGCCCGGTGTCTGAGGAACTCCAGCTGGGCCCGCAGAGATTCGACGGGGAATCCA        | 389  |
| Qy  | 301  | AGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCCGTTAGCT      | 360  |
| Db  | 390  | AGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCCGTTAGCT      | 449  |
| Qy  | 361  | GGCCACGATATCACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAGTGT     | 420  |
| Db  | 450  | GGCCACGATATCACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAGTGT     | 509  |
| Qy  | 421  | GAGATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGTGTGTGGCTTATGTGT        | 480  |
| Db  | 510  | GAGATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGTGTGTGGCTTATGTGT        | 569  |
| Qy  | 481  | GCACTGGGCAATTAATGGCTCTTTTTCACCGCACACGCACTGGCAAGGGTCAGTCAAT     | 540  |
| Db  | 570  | GCACTGGGCAATTAATGGCTCTTTTTCACCGCACACGCACTGGCAAGGGTCAGTCAAT     | 629  |
| Qy  | 541  | GATGCAAAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGTGTGAAACTCAGAAA    | 600  |
| Db  | 630  | GATGCAAAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGTGTGAAACTCAGAAA    | 689  |
| Qy  | 601  | TCGAGCTGTGGGAGGACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTCTAT       | 660  |
| Db  | 690  | TCGAGCTGTGGGAGGACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTCTAT       | 749  |
| Qy  | 661  | ACGACTTACAGACACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC      | 720  |
| Db  | 750  | ACGACTTACAGACACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC      | 809  |
| Qy  | 721  | TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC | 780  |
| Db  | 810  | TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC | 869  |
| Qy  | 781  | ATGGATGATTTGCCAGGAATGAGAGAGTTTGCAGATGTTATTTGCAAGAGACGAG        | 840  |
| Db  | 870  | ATGGATGATTTGCCAGGAATGAGAGAGTTTGCAGATGTTATTTGCAAGAGACGAG        | 929  |
| Qy  | 841  | GCAGAGTGTGTCAAAATCTTTTCACCGCACAGATGCTGTGACTCCGGTCTCGACTTTT     | 900  |
| Db  | 930  | GCAGAGTGTGTCAAAATCTTTTCACCGCACAGATGCTGTGACTCCGGTCTCGACTTTT     | 989  |
| Qy  | 901  | GAGGAGTGTGTTCATCATGATCACAAAGGAAACCGGGCTCGTTTATCACAGTGAAGAG     | 960  |
| Db  | 990  | GAGGAGTGTGTTCATCATGATCACAAAGGAAACCGGGCTCGTTTATCACAGTGAAGAG     | 1049 |
| Qy  | 961  | CAGGAGCTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTCTTTC      | 1020 |
| Db  | 1050 | CAGGAGCTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTCTTTC      | 1109 |
| Qy  | 1021 | AAAGGGATTCCTTTTATAGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTCAGC  | 1080 |
| Db  | 1110 | AAAGGGATTCCTTTTATAGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTCAGC  | 1169 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1081 | CGCGAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTATAAAGGTAAAGCT | 1140 |
| Db | 1170 | CGCGAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTATAAAGGTAAAGCT | 1229 |
| Qy | 1141 | AGTCTC 1146  |      |
| Db | 1230 | AGTCTC 1235  |      |

RESULT 6  
ADB75193  
ID ADB75193 standard; cDNA; 2069 BP.  
XX ADB75193;  
XX 04-DEC-2003 (first entry)  
XX Prostate cancer marker cDNA.  
XX Prostate; cancer; cytostatic; gene therapy; marker; ss.  
XX Homo sapiens.  
XX WO2003009814-A2.  
XX 06-FEB-2003.  
XX 25-JUL-2002; 2002WO-US023913.  
XX 25-JUL-2001; 2001US-0307982P.  
XX 22-AUG-2001; 2001US-0314356P.  
XX 25-SEP-2001; 2001US-0325020P.  
XX 12-DEC-2001; 2001US-0341746P.  
XX 05-MAR-2002; 2002US-0362158P.  
(MILL-) MILLENNIUM PHARM INC.

Schlegel R, Monahan JF, Endege WO, Gannavarapu M, Gorbacheva B;  
Hoerish S, Kamatkar S, Wonsey AM, Glatk K, Zhao X, Anderson D;  
WPI; 2003-248033/24.  
New nucleic acid molecule, useful for diagnosing or treating prostate cancer.

Claim 1; SEQ ID NO 17; 99pp; English.

The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 U; 0 Other;

|                       |                 |               |           |              |
|-----------------------|-----------------|---------------|-----------|--------------|
| Query Match           | 100.0%;         | Score 1146;   | DB 10;    | Length 2069; |
| Best Local Similarity | 100.0%;         | Pred. No. 0;  |           |              |
| Matches 1146;         | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0;      |

|    |    |   |     |
|----|----|---|-----|
| Qy | 1  | ATGGCACTGCAGGGGATCTCGGTGTGTGAGCTGTCCGGCTGTGGCCCGGGCCCGTTCGT | 60  |
| Db | 90 | ATGGCACTGCAGGGGATCTCGGTGTGTGAGCTGTCCGGCTGTGGCCCGGGCCCGTTCGT | 149 |

QY 61 GCTATGGTCTGCTGACCTTCGGGGGGCGGTGTGGTACGGGTGGACCGGGCCGGCTCCCGC 120  
 Db |||||  
 QY 121 TACGACGTGAGCGCTTGGGGCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCGG 180  
 Db |||||  
 QY 210 TACGACGTGAGCGCTTGGGGCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCGG 269  
 Db |||||  
 QY 181 CGGGAGCGCGCTGCTGCGGGCTCTGTGCAAGCGGTGGATGTCTGTGAGCCCTTC 240  
 Db |||||  
 QY 270 CGGGAGCGCGCTGCTGCGGGCTCTGTGCAAGCGGTGGATGTCTGTGAGCCCTTC 329  
 Db |||||  
 QY 241 CGCGGGGTGTCATGAGAACTCCAGCTGGGCCCGCAGAGATTCTCGACGGGGAATCCA 300  
 Db |||||  
 QY 330 CGCGCGGTGTATGAGAACTCCAGCTGGGCCCGCAGAGATTCTCGACGGGGAATCCA 389  
 Db |||||  
 QY 301 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCGCGGTTAGCT 360  
 Db |||||  
 QY 390 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCGCGGTTAGCT 449  
 Db |||||  
 QY 361 GCGCACGATATCACTATTGGCTTTGTGAGGTGTTCTCAAAATTTGGCAGAGTGGT 420  
 Db |||||  
 QY 450 GCGCACGATATCACTATTGGCTTTGTGAGGTGTTCTCAAAATTTGGCAGAGTGGT 509  
 Db |||||  
 QY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTT 480  
 Db |||||  
 QY 510 GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTT 569  
 Db |||||  
 QY 481 GCACCTGGGCAATTATAGCTCTTTTTCACCGCACCGCTGCGCAAGGCTCAGTCAAT 540  
 Db |||||  
 QY 570 GCACCTGGGCAATTATAGCTCTTTTTCACCGCACCGCTGCGCAAGGCTCAGTCAAT 629  
 Db |||||  
 QY 541 GATCAAAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGCAAACTCAGAAA 600  
 Db |||||  
 QY 630 GATGCAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGCAAACTCAGAAA 689  
 Db |||||  
 QY 601 TCGAGTGTGTGGAGAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTTCTAT 660  
 Db |||||  
 QY 690 TCGAGTGTGTGGAGAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTTCTAT 749  
 Db |||||  
 QY 661 AGCACTTACAGACAGCAGATGGGAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 720  
 Db |||||  
 QY 750 AGCACTTACAGACAGCAGATGGGAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 809  
 Db |||||  
 QY 721 TACGAGCTGCTGATCAAGAGCTTGGACTTAAAGTCTGATGAATTCCTCAATCAGATGAGC 780  
 Db |||||  
 QY 810 TACGAGCTGCTGATCAAGAGCTTGGACTTAAAGTCTGATGAATTCCTCAATCAGATGAGC 869  
 Db |||||  
 QY 781 ATGGATGATTGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGAAAGACGAAAG 840  
 Db |||||  
 QY 870 ATGGATGATTGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGAAAGACGAAAG 929  
 Db |||||  
 QY 841 GCAGAGTGTGTCAAACTTTTACCGGACAGATGCTGTGACATCCCGGTTCTGACTTTT 900  
 Db |||||  
 QY 930 GCAGAGTGTGTCAAACTTTTACCGGACAGATGCTGTGACATCCCGGTTCTGACTTTT 989  
 Db |||||  
 QY 901 GAGGAGTGTGTTCATCATGATCACAAAGGAACCGGGCTCGTTTATCACCAGTGAGGAG 960  
 Db |||||  
 QY 990 GAGGAGTGTGTTCATCATGATCACAAAGGAACCGGGCTCGTTTATCACCAGTGAGGAG 1049  
 Db |||||  
 QY 961 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTGTTAAACACCCAGCCATCCCTTCTTTC 1020  
 Db |||||  
 QY 1050 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTGTTAAACACCCAGCCATCCCTTCTTTC 1109  
 Db |||||  
 QY 1021 AAAAGGATTCCTTTTCATAGGAGAAACACTGAGGAGATCACTTGAAGAAATTTGGATTCAGC 1080  
 Db |||||  
 QY 1110 AAAAGGATTCCTTTTCATAGGAGAAACACTGAGGAGATCACTTGAAGAAATTTGGATTCAGC 1169  
 Db |||||  
 QY 1081 CCGGAGGATTTATCAGCTTAACTCAGTAAATCAATTTGAAGTAATTAAGTAAAGCT 1140  
 Db |||||  
 QY 1170 CCGGAGGATTTATCAGCTTAACTCAGTAAATCAATTTGAAGTAATTAAGTAAAGCT 1229  
 Db |||||

QY 1141 AGTCTC 1146  
 Db 1230 AGTCTC 1235  
 RESULT 7  
 AAD38605  
 ID AAD38605 standard; cDNA; 3654 BP.  
 XX AAD38605;  
 AC  
 XX 23-SEP-2002 (first entry)  
 XX Human alpha-methylacyl-CoA racemase splice variant, SV2 cDNA.  
 DE Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;  
 KW cytostatic; SV2; gene; ss.  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 CDS 90..1274  
 FT /\*tag= a  
 FT /product= "Human SV2 protein"  
 FT /transl\_except= (pos:612..614, aa:Asp)  
 XX  
 PN WO20227324-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 28-SEP-2001; 2001WO-US030532.  
 XX  
 PR 28-SEP-2000; 2000US-0236238P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Richardson J, Monahan J;  
 XX  
 DR WPI; 2002-405070/43.  
 XX  
 DR P-PSDB; AAE23973.  
 XX  
 PT Determining risk for prostate cancer in subject or risk for metastatic  
 prostate cancer to liver or lymph nodes of prostate cancer patients,  
 comprises measuring expression or activity of alpha-methylacyl-CoA  
 racemase.  
 XX  
 PS Claim 54; Fig 5; 102pp; English.  
 XX  
 CC The present invention relates to novel methods for determining whether an  
 individual is at risk for prostate cancer or whether a prostate cancer  
 patient is at risk for metastatic prostate cancer to the liver or lymph  
 nodes. The method involves measuring the expression or activity of alpha-  
 methylacyl-CoA racemase. Sequences of the invention are useful in  
 CC diagnostic methods, drug screening assays, and in treating or preventing  
 cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-  
 acyl-CoA racemase splice variant, SV2 cDNA  
 XX  
 SQ Sequence 3654 BP; 1050 A; 751 C; 888 G; 965 T; 0 U; 0 Other;  
 Query Match 98.8%; Score 1132; DB 6; Length 3654;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGGCACTGCAGGCACTCTCGGTCTGAGCTGTCCGGCTTGGCCCGGCCCTTCTGT 60  
 Db |||||  
 QY 90 ATGGCACTGCAGGCACTCTCGGTCTGAGCTGTCCGGCTTGGCCCGGCCCTTCTGT 149  
 Db |||||  
 QY 61 GCTATGTTCTGGCTGACTTCGGGGCGCGTGTGTAGCGTGGACCGCCCGGCTCCCGC 120  
 Db |||||  
 QY 150 GCTATGTTCTGGCTGACTTCGGGGCGCGTGTGTAGCGTGGACCGCCCGGCTCCCGC 209  
 Db |||||  
 QY 121 TACGACGTGAGCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCG 180  
 Db |||||

Db 210 TACGACGTGAGCCGCTTGGCGGGCAAGCGCTCGCTAGTGTCTGAGACCTGAAGCAGCG 269  
QY 181 CGGGAGCCGCGCTGCTGCGCGCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 240  
Db 270 CGGGAGCCGCGCTGCTGCGCGCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 329  
QY 241 CGCGCGGTGTCTGGAGAAACTCCAGCTGGCGCCAGAGATTCTGCAGCGGGAATAATCCA 300  
Db 330 CGCGCGGTGTCTGGAGAAACTCCAGCTGGCGCCAGAGATTCTGCAGCGGGAATAATCCA 389  
QY 301 AGGCTTATTATGACGAGCTGAGTGGATTGGCCAGTCAGGAATCTTGCCTGGTTAGCT 360  
Db 390 AGGCTTATTATGACGAGCTGAGTGGATTGGCCAGTCAGGAATCTTGCCTGGTTAGCT 449  
QY 361 GGCCACGATATCACTATTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGT 420  
Db 450 GGCCACGATATCACTATTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGT 509  
QY 421 GAGAACTCGATGCCCGCTGAATCTCTGCTGCTGACTTTGTGCTGGTGGCTTTATGT 480  
Db 510 GAGAACTCGATGCCCGCTGAATCTCTGCTGCTGACTTTGTGCTGGTGGCTTTATGT 569  
QY 481 GCATGGGCATTATAATGGCTCTTTTGAACGACACGACACTGGCAAGGTCAGGTCA 540  
Db 570 GCATGGGCATTATAATGGCTCTTTTGAACGACACGACACTGGCAAGGTCAGGTCA 629  
QY 541 GATGCAATATGGTGAAGGACACGATATTTAAGTCTTTTCTGTGGAATACTCAGAA 600  
Db 630 GATGCAATATGGTGAAGGACACGATATTTAAGTCTTTTCTGTGGAATACTCAGAA 689  
QY 601 TCGAGTCTGTGGAGACACCTCGAGGACAGAACATGTTGGATGTTGGAGCACTTTCTAT 660  
Db 690 TCGAGTCTGTGGAGACACCTCGAGGACAGAACATGTTGGATGTTGGAGCACTTTCTAT 749  
QY 661 ACAGCTTACAGGACACGACAGATGGGAAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 720  
Db 750 ACAGCTTACAGGACACGACAGATGGGAAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 809  
QY 721 TACGAGCTGTGATCAAAAGGACTTGGACTAAGTCTGATGAATCTCCCAATCAGATGAGC 780  
Db 810 TACGAGCTGTGATCAAAAGGACTTGGACTAAGTCTGATGAATCTCCCAATCAGATGAGC 869  
QY 781 ATGAGTATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTGCAAGAACGCAAG 840  
Db 870 ATGAGTATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTGCAAGAACGCAAG 929  
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGACTTTT 900  
Db 930 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGACTTTT 989  
QY 901 GAGGAGTGTTCATCATGATCACAACAGGAACGGGCTGTTTATCACCAGTGAGGAG 960  
Db 990 GAGGAGTGTTCATCATGATCACAACAGGAACGGGCTGTTTATCACCAGTGAGGAG 1049  
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1020  
Db 1050 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1109  
QY 1021 AAAAGGATCTCTTTTCATAGGAGAACACACTCAGGAGATACCTTGAAGATTTGGATTACG 1080  
Db 1110 AAAAGGATCTCTTTTCATAGGAGAACACACTCAGGAGATACCTTGAAGATTTGGATTACG 1169  
QY 1081 CGCGAAGAGATTTATCAGCTTAATCTCAGATATAAATCATTTGAAGTAATTAAGG 1132  
Db 1170 CGCGAAGAGATTTATCAGCTTAATCTCAGATATAAATCATTTGAAGTAATTAAGG 1221

RESULT 8  
ADB75195  
ID ADB75195 standard; cDNA; 3654 BP.  
XX  
AC ADB75195;  
XX

DT 04-DEC-2003 (first entry)  
XX Prostate cancer marker cDNA.  
XX Prostate; cancer; cytostatic; gene therapy; marker; ss.  
XX Homo sapiens.  
XX W02003009814-A2.  
XX 06-FEB-2003.  
XX 25-JUL-2002; 2002WO-US023913.  
XX 25-JUL-2001; 2001US-0307982P.  
XX 22-AUG-2001; 2001US-0314356P.  
XX 25-SEP-2001; 2001US-0325020P.  
XX 12-DEC-2001; 2001US-0341746P.  
XX 05-MAR-2002; 2002US-0362158P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Schlegel R, Monahan JB, Endege WO, Gannavarapu M, Gorbacheva B;  
XX Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;  
XX WPI; 2003-248033/24.  
XX New nucleic acid molecule, useful for diagnosing or treating prostate  
XX cancer.  
XX Claim 1; SEQ ID NO 19; 99pp; English.  
XX The invention relates to newly discovered cancer markers associated with  
XX the cancerous state of prostate cells. Also disclosed is a method of  
XX assessing whether a patient is afflicted with prostate cancer. The method  
XX of the invention involves assessing whether a patient is afflicted with  
XX prostate cancer by comparing the level of expression of a marker in a  
XX patient sample and the normal level of expression of the marker in a  
XX control non-prostate cancer sample, where a significant increase in the  
XX level of expression of the marker in the patient sample and the normal  
XX level indicates that the patient is afflicted with prostate cancer.  
XX Nucleic acids of the invention are useful for diagnosing or treating  
XX prostate cancer, and may be useful in gene therapy. Sequences given in  
XX ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 3654 BP; 1050 A; 751 C; 888 G; 965 T; 0 U; 0 Other;  
  
Query Match 98.8%; Score 1132; DB 10; Length 3654;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGCACTGCAGGCACTTCGGTCTGGAGCTGTCGGCCCTCGGCCCGCGGCTTCTGT 60  
Db 90 ATGCACTGCAGGCACTTCGGTCTGGAGCTGTCGGCCCTCGGCCCGCGGCTTCTGT 149  
  
QY 61 GCTATGCTCTGGCTGACTTTCGGGGCCGCTGTGTACGCGTGGACCGCGGCTCCCGC 120  
Db 150 GCTATGCTCTGGCTGACTTTCGGGGCCGCTGTGTACGCGTGGACCGCGGCTCCCGC 209  
  
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAACACCG 180  
Db 210 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGCTGGACCGCG 269  
  
QY 181 CGGGAGCCGCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGAGCCCTTC 240  
Db 270 CGGGAGCCGCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGAGCCCTTC 329  
  
QY 241 CGCCCGGTGTCTATGGAGAAATCTCCAGCTGGGCGCCAGAGATTTCTGCAGCGGGAATAATCCA 300  
Db 330 CGCCCGGTGTCTATGGAGAAATCTCCAGCTGGGCGCCAGAGATTTCTGCAGCGGGAATAATCCA 389



Qy 421 GAGAAATCGTATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGGCTTATGTGT 480  
Db |||||  
Qy 510 GAGAAATCGTATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGGCTTATGTGT 569  
Db |||||  
Qy 481 GCACCTGGGCATTAATATGGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGGTCAAT 540  
Db |||||  
Qy 570 GCACCTGGGCATTAATATGGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGGTCAAT 629  
Db |||||  
Qy 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTCTTTTCTGTGGAACATCAGAAA 600  
Db |||||  
Qy 630 GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTCTTTTCTGTGGAACATCAGAAA 689  
Db |||||  
Qy 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGCTGGAGCACCTTTCTAT 660  
Db |||||  
Qy 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGCTGGAGCACCTTTCTAT 749  
Db |||||  
Qy 661 ACGACTTACAGGACAGGAGTGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720  
Db |||||  
Qy 750 ACGACTTACAGGACAGGAGTGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 809  
Db |||||  
Qy 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780  
Db |||||  
Qy 810 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 869  
Db |||||  
Qy 781 ATGGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAAAAGAACGAAAG 840  
Db |||||  
Qy 870 ATGGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAAAAGAACGAAAG 929  
Db |||||  
Qy 841 GCAGAGTGGTCAAAATCTTTGACGGGCACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db |||||  
Qy 930 GCAGAGTGGTCAAAATCTTTGACGGGCACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 989  
Db |||||  
Qy 901 GAGGAGGTGTTTCATCATGATCACAACAAGGAACGGGGCTGTTTATCACCAGTGAGGAG 960  
Db |||||  
Qy 990 GAGGAGGTGTTTCATCATGATCACAACAAGGAACGGGGCTGTTTATCACCAGTGAGGAG 1049  
Db |||||  
Qy 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1020  
Db |||||  
Qy 1050 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1109  
Db |||||  
Qy 1021 AAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTCAGC 1080  
Db |||||  
Qy 1110 AAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTCAGC 1169  
Db |||||  
Qy 1081 CGCGAGAGATTTATCAGCTTAATCTCAGATAAAATCATTGAAGTAAATAGGTAAGAGCT 1140  
Db |||||  
Qy 1170 CGCGAAGAGATTTATCAGCTTAATCTCAGATAAAATCATTGAAGTAAATAGGTAAGAGCT 1229  
Db |||||  
Qy 1141 AGTCTC 1146  
Db |||||  
Qy 1230 AGTCTC 1235  
Db |||||

RESULT 10  
ADB75203  
ID ADB75203 standard; cDNA; 2626 BP.

XX ADB75203;

XX 04-DEC-2003 (first entry)

XX Prostate cancer marker cDNA.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Homo sapiens.

XX WO2003009814-A2.

XX 06-FEB-2003.

XX 25-JUL-2002; 2002WO-US023913.

PR 25-JUL-2001; 2001US-0307982P.  
PR 22-AUG-2001; 2001US-0314356P.  
PR 25-SEP-2001; 2001US-0325020P.  
PR 12-DEC-2001; 2001US-0341746P.  
PR 05-MAR-2002; 2002US-0362158P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;  
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;  
XX WPI; 2003-248033/24.  
DR New nucleic acid molecule, useful for diagnosing or treating prostate  
XX cancer.  
PS Claim 1; SEQ ID NO 27; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with  
CC the cancerous state of prostate cells. Also disclosed is a method of  
CC assessing whether a patient is afflicted with prostate cancer. The method  
CC of the invention involves assessing whether a patient is afflicted with  
CC prostate cancer by comparing the level of expression of a marker in a  
CC patient sample and the normal level of expression of the marker in a  
CC control non-prostate cancer sample, where a significant increase in the  
CC level of expression of the marker in the patient sample and the normal  
CC level indicates that the patient is afflicted with prostate cancer.  
CC Nucleic acids of the invention are useful for diagnosing or treating  
CC prostate cancer, and may be useful in gene therapy. Sequences given in  
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 2626 BP; 697 A; 573 C; 664 G; 692 T; 0 U; 0 Other;

Query Match 94.3%; Score 1081; DB 10; Length 2626;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCACTGACGGGCATCTCGGTCTGGAGCTGTCGGGCTGGCCCGGCTTCTGT 60  
Db |||||  
Qy 61 GCTATGCTCTGCTGACTTTCGGGGCGGCTGTGTAGCGTGACCGGCGGCTCCCGC 120  
Db |||||  
Qy 150 GCTATGCTCTGCTGACTTTCGGGGCGGCTGTGTAGCGTGACCGGCGGCTCCCGC 209  
Db |||||  
Qy 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCG 180  
Db |||||  
Qy 210 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCG 269  
Db |||||  
Qy 181 CGGGAGCCGCGGTGCTGCGGCGGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240  
Db |||||  
Qy 270 CGGGAGCCGCGGTGCTGCGGCGGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 329  
Db |||||  
Qy 241 CGCGCGGTGCTCATGGAGAACTCCAGCTGGGCGCCAGAGATTCGCGAGCGGGAATCCA 300  
Db |||||  
Qy 330 CGCGCGGTGCTCATGGAGAACTCCAGCTGGGCGCCAGAGATTCGCGAGCGGGAATCCA 389  
Db |||||  
Qy 301 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 360  
Db |||||  
Qy 390 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 449  
Db |||||  
Qy 361 GGCCACGATATCAACTATTTGGCTTTTGTCAAGGTTTCTCAAAAAATTTGGCAGAGTGT 420  
Db |||||  
Qy 450 GGCCACGATATCAACTATTTGGCTTTTGTCAAGGTTTCTCAAAAAATTTGGCAGAGTGT 509  
Db |||||  
Qy 421 GAGNAATCGGTATGCCCGCTGAAATCTCTGGCTGACTTTCGCTGGTGGGCTTATGTGT 480  
Db |||||  
Qy 510 GAGNAATCGGTATGCCCGCTGAAATCTCTGGCTGACTTTCGCTGGTGGGCTTATGTGT 569  
Db |||||  
Qy 481 GCACCTGGGCATTAATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGTCAAT 540  
Db |||||

Db 570 GCACCTGGCATATTAATGGCTCTTTTGACCGCACACGCACTGACAAAGGTCAGTCAATT 629  
 Qy 541 GATGCAAAATATGGTGGAAAGCAACAGCATATTTAAAGTTCTTTTCTGTGGAAACTCAGAAA 600  
 Db 630 GATGCAAAATATGGTGGAAAGCAACAGCATATTTAAAGTTCTTTTCTGTGGAAACTCAGAAA 689  
 Qy 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTTCTAT 660  
 Db 690 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTTCTAT 749  
 Qy 661 ACAGCTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720  
 Db 750 ACAGCTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 809  
 Qy 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780  
 Db 810 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 869  
 Qy 781 ATGGATGATGGCCAGAAATGAAGAAAGTTTGAGATGTTTGCAAGAAAGCAAG 840  
 Db 870 ATGGATGATGGCCAGAAATGAAGAAAGTTTGAGATGTTTGCAAGAAAGCAAG 929  
 Qy 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGACTTTT 900  
 Db 930 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGACTTTT 989  
 Qy 901 GAGGAGGTTGTTCAATCATGATCACAACAAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 960  
 Db 990 GAGGAGGTTGTTCAATCATGATCACAACAAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 1049  
 Qy 961 CAGGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCCAAGCAATCCCTTCTTTC 1020  
 Db 1050 CAGGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCCAAGCAATCCCTTCTTTC 1109  
 Qy 1021 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAGAAATTTGGATTTCAGC 1080  
 Db 1110 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAGAAATTTGGATTTCAGC 1169  
 Qy 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGG 1132  
 Db 1170 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGG 1221

RESULT 11  
 AAV58584  
 ID AAV58584 standard; cDNA; 1621 BP.  
 XX AC AAV58584;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 08-DEC-1998 (first entry)  
 XX DE Prostate tumour specific gene clone P1-12.  
 XX KW Prostate tumour specific gene; human; prostate cancer; detection;  
 XX KW therapy; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT CDS 5..1153  
 XX FT /\*tag= a  
 XX PN W09837418-A2.  
 XX PD 27-AUG-1998.  
 XX PF 25-FEB-1998; 98WO-US003690.  
 XX PR 25-FEB-1997; 97US-00806596.  
 XX PR 01-AUG-1997; 97US-00904809.  
 XX PR 09-FEB-1998; 98US-00020747.

XX (CORI-) CORIXA CORP.  
 XX Xu J, Dillon DC;  
 XX WPI: 1998-480805/41.  
 XX P-PSDB; AAW69383.  
 XX Novel human prostate specific tumour protein and fragments - useful for  
 XX detecting and treating prostate cancers.  
 XX Claim 1; Page 81-82; 141pp; English.  
 XX This sequence represents a human prostate tumour specific gene, and can  
 XX be used in the method of the invention. The method is for detecting  
 XX prostate cancer comprising contacting a biological sample with an agent  
 XX able to bind an immunogenic portion of a prostate protein (such as  
 XX encoded by this sequence). An antibody which binds to an immunogenic  
 XX portion of the prostate protein, and the method can be used to detect,  
 XX monitor progression of, or treat prostate cancers. The antibody may also  
 XX be conjugated to a therapeutic agent for use in therapy of prostate  
 XX cancers. (Updated on 25-MAR-2003 to correct PR field.)  
 XX SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;  
 Query Match 93.4%; Score 1070; DB 2; Length 1621;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 26 TGGAGCTGTCGGGCTGGCCCGGGCCGCTCTCTGCTATGCTTGGCTGACTTCGGGG 85  
 Db 30 TGGAGCTGTCGGGCTGGCCCGGGCCGCTCTCTGCTATGCTTGGCTGACTTCGGGG 89  
 Qy 86 CGCGTGTGTACGCTGGACCGCGCCCGCTCCCGCTACGAGCTGAGCCGCTTGGCCCGGG 145  
 Db 90 CGCGTGTGTACGCTGGACCGCGCCCGCTCCCGCTACGAGCTGAGCCGCTTGGCCCGGG 149  
 Qy 146 GCAAGCGCTCGTGTAGTCTGGAACCTGAAGCAGCCCGGGAGCCCGCTGTGCGGCGTC 205  
 Db 150 GCAAGCGCTCGTGTAGTCTGGAACCTGAAGCAGCCCGGGAGCCCGCTGTGCGGCGTC 209  
 Qy 206 TGTCAACCGCTCGGATGTGCTGAGCCCTTCCCGCGGGTGTCAAGAGAACTCC 265  
 Db 210 TGTCAACCGCTCGGATGTGCTGAGCCCTTCCCGCGGGTGTCAAGAGAACTCC 269  
 Qy 266 AGCTGGGCCAGAGATTTCTGAGCGGGAATCAAGGCTTTATTTATGCCAGGCTGAGTG 325  
 Db 270 AGCTGGGCCAGAGATTTCTGAGCGGGAATCAAGGCTTTATTTATGCCAGGCTGAGTG 329  
 Qy 326 GATTTGGCCAGTCAAGGAGCTTTGCGCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 385  
 Db 330 GATTTGGCCAGTCAAGGAGCTTTGCGCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 389  
 Qy 386 TGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGTGAGAAATCCGATGCCCGCTGAATC 445  
 Db 390 TGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGTGAGAAATCCGATGCCCGCTGAATC 449  
 Qy 446 TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGTGCACTGGCATTAATATGCTCTTT 505  
 Db 450 TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGTGCACTGGCATTAATATGCTCTTT 509  
 Qy 506 TTGACCGCACACGCACTGGCAAGGTCAGGTCATTGTATGCAAAATATGTTGGAAGCAACAG 565  
 Db 510 TTGACCGCACACGCACTGGCAAGGTCAGGTCATTGTATGCAAAATATGTTGGAAGCAACAG 569  
 Qy 566 CATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGAGCACTTCGAG 625  
 Db 570 CATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGAGCACTTCGAG 629  
 Qy 626 GACAGAAATGTTGGATGGTGGAGCACTTTCTATAGACTTTACAGGACAGCATGGGG 685  
 Db 630 GACAGAAATGTTGGATGGTGGAGCACTTTCTATAGACTTTACAGGACAGCATGGGG 689



|  |    |      |  |      |
|--|----|------|--|------|
|  | Qy | 686  | AATTCAATGGCTGTTGGAGCAATAAGAACCCCGAGTTCACGAGCTCCTCATCAAAGGACTTG | 745  |
|  | Db | 690  | AATTCAATGGCTGTTGGAGCAATAAGAACCCCGAGTTCACGAGCTCCTCATCAAAGGACTTG | 749  |
|  | Qy | 746  | GACTAAAGTCTGATGAACCTCCCNAATCAGATGAGCATGGATGATTGGCAGAAAATGAAGA  | 805  |
|  | Db | 750  | GACTAAAGTCTGATGAACCTCCCNAATCAGATGAGCATGGATGATTGGCAGAAAATGAAGA  | 809  |
|  | Qy | 806  | AGAAATTTGCAGATGTATTTGCCAAAGACGAAAGGCAGAGTGGTGTCAAATCTTTGACG    | 865  |
|  | Db | 810  | AGAAATTTGCAGATGTATTTGCCAAAGACGAAAGGCAGAGTGGTGTCAAATCTTTGACG    | 869  |
|  | Qy | 866  | GCACAGATGCTGTGTCACCTCCGGTCTGACTTTTGGAGGAGTGTTCATCATGATCACACA   | 925  |
|  | Db | 870  | GCACAGATGCTGTGTCACCTCCGGTCTGACTTTTGGAGGAGTGTTCATCATGATCACACA   | 929  |
|  | Qy | 926  | ACAAGGAACGGGGCTCGTTTTATCACAGTGAGGAGCAGGACGTCGAGCCCCCGCCCTGCAC  | 985  |
|  | Db | 930  | ACAAGGAACGGGGCTCGTTTTATCACAGTGAGGAGCAGGACGTCGAGCCCCCGCCCTGCAC  | 989  |
|  | Qy | 986  | CTCTGCTGTTAAACACCCECCAGCCATCCCTCTTTCAAAGGGATCCTTTTCATAGGAGAAC  | 1045 |
|  | Db | 990  | CTCTGCTGTTAAACACCCECCAGCCATCCCTCTTTCAAAGGGATCCTTTTCATAGGAGAAC  | 1049 |
|  | Qy | 1046 | ACACTGAGGAGATACTTTGAAGAAATTTGGATTCAGCCCGAAGAGATTTATCAGCTTAACT  | 1105 |
|  | Db | 1050 | ACACTGAGGAGATACTTTGAAGAAATTTGGATTCAGCCCGAAGAGATTTATCAGCTTAACT  | 1109 |
|  | Qy | 1106 | CAGATAAAATCATTTGAAAGTAATAAGGTAAAAAGCTAGTCTC                    | 1146 |
|  | Db | 1110 | CAGATAAAATCATTTGAAAGTAATAAGGTAAAAAGCTAGTCTC                    | 1150 |

## RESULT 12

AAV61199

AAV61199  
ID AAV61199 standard: cDNA: 1621 BP.

AA AAV61199:

XX  
DT 06-JAN-1999 (first entry)

DE Full length cDNA sequence of prostate tumour clone F1-12.

KW prostate: cancer: tumour: vaccine: immunogen: clone: ss.

XX  
OS  
Homo sapiens.XX  
PW  
WQ9837093-A2XX  
27-AUG-1998

XX  
PF 25-FEB-1998. 09W0-IIS003492

XX  
25-538-1007. 0710-00000000

PR 01-AUG-1997; 97US-00904804.  
 PR 09-FEB-1999. 99US-00020956

XX  
DA  
(CONT.)  
CORP  
CORP  
CORP

XX

XX

DR P-PSDB; AAW71867.

PT polypeptides comp

PS Claim 3; Page 76-77; 130pp; English.

CC The present sequence is a new DNA wh

CC a prostate tumour protein, the encoded immunogen, of the DNA itself, can  
CC be used as a vaccine for the treatment of prostate cancer. The DNA was  
CC identified by analysis of a subtracted cDNA library obtained by









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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 02:32:35 ; Search time 5147 Seconds  
(without alignments)  
10788.746 Million cell updates/sec

Title: US-09-967-305-3  
Perfect score: 1146  
Sequence: 1 atggcactgcaggcatctc.....ataaggtaaagtagtctc 1146

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

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- 2: gb\_hg.\*
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- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sv.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description        |
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| 1          | 1146  | 100.0         | 1146   | 6  | AX497154 Sequence  |
| 2          | 1146  | 100.0         | 2005   | 6  | AX497152 Sequence  |
| 3          | 1146  | 100.0         | 2005   | 6  | AX497161 Sequence  |
| 4          | 1146  | 100.0         | 2005   | 9  | AF158378 Homo sapi |
| 5          | 1146  | 100.0         | 2069   | 6  | AX497155 Sequence  |
| 6          | 1132  | 98.8          | 3654   | 6  | AX497157 Sequence  |
| 7          | 1070  | 93.4          | 1621   | 6  | BD242020 Compounds |
| 8          | 1070  | 93.4          | 1621   | 6  | AR237203 Sequence  |
| 9          | 1070  | 93.4          | 1621   | 6  | AR278227 Sequence  |
| 10         | 1070  | 93.4          | 1621   | 6  | AR366923 Sequence  |
| 11         | 1070  | 93.4          | 1621   | 6  | AR370819 Sequence  |
| 12         | 1070  | 93.4          | 1621   | 6  | AR392324 Sequence  |
| 13         | 1070  | 93.4          | 1621   | 6  | AR399959 Sequence  |
| 14         | 1070  | 93.4          | 1621   | 6  | AR405226 Sequence  |
| 15         | 1070  | 93.4          | 1621   | 6  | AR439430 Sequence  |
| 16         | 1070  | 93.4          | 1621   | 6  | AR563606 Sequence  |
| 17         | 1070  | 93.4          | 1621   | 6  | AX106326 Sequence  |
| 18         | 1070  | 93.4          | 1621   | 6  | AX140617 Sequence  |
| 19         | 1070  | 93.4          | 1621   | 6  | AX200477 Sequence  |

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| 20 | 1070 | 93.4 | 1621 | 6 | AX267133 | AX267133 Sequence  |
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| 22 | 1070 | 93.4 | 2045 | 6 | CQ726257 | CQ726257 Sequence  |
| 23 | 1070 | 93.4 | 2376 | 6 | CQ489417 | CQ489417 Sequence  |
| 24 | 1070 | 93.4 | 2376 | 6 | CQ490005 | CQ490005 Sequence  |
| 25 | 1070 | 93.4 | 2376 | 6 | CQ493361 | CQ493361 Sequence  |
| 26 | 1070 | 93.4 | 2376 | 6 | CQ495259 | CQ495259 Sequence  |
| 27 | 1019 | 88.9 | 1674 | 6 | BD155688 | BD155688 Primer fo |
| 28 | 1019 | 88.9 | 1674 | 6 | AX875662 | AX875662 Sequence  |
| 29 | 1019 | 88.9 | 1674 | 9 | AK000912 | AK000912 Homo sapi |
| 30 | 866  | 75.6 | 2041 | 9 | AF047020 | AF047020 Homo sapi |
| 31 | 797  | 69.5 | 1294 | 6 | CQ490746 | CQ490746 Sequence  |
| 32 | 797  | 69.5 | 1294 | 6 | CQ490859 | CQ490859 Sequence  |
| 33 | 797  | 69.5 | 1294 | 6 | CQ495858 | CQ495858 Sequence  |
| 34 | 797  | 69.5 | 1294 | 6 | CQ496588 | CQ496588 Sequence  |
| 35 | 797  | 69.5 | 1294 | 6 | CQ496690 | CQ496690 Sequence  |
| 36 | 756  | 66.0 | 1039 | 6 | AX593026 | AX593026 Sequence  |
| 37 | 672  | 58.6 | 858  | 9 | AV330489 | AV330489 Homo sapi |
| 38 | 613  | 53.5 | 1317 | 6 | BD159629 | BD159629 Primer fo |
| 39 | 613  | 53.5 | 1317 | 6 | AX882271 | AX882271 Sequence  |
| 40 | 613  | 53.5 | 1317 | 9 | AK022765 | AK022765 Homo sapi |
| 41 | 595  | 51.9 | 2946 | 9 | BC009471 | BC009471 Homo sapi |
| 42 | 595  | 51.9 | 3023 | 6 | AX497159 | AX497159 Sequence  |
| 43 | 524  | 45.7 | 720  | 6 | BD145333 | BD145333 Primer fo |
| 44 | 524  | 45.7 | 720  | 6 | AX865271 | AX865271 Sequence  |
| 45 | 493  | 43.0 | 865  | 6 | CQ488657 | CQ488657 Sequence  |

ALIGNMENTS

RESULT 1  
AX497154  
LOCUS AX497154 1146 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 3 from Patent WO0227324.  
ACCESSION AX497154  
VERSION AX497154.1 GI:23342546  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Richardson, J.  
TITLE Alpha-methylacyl-coa racemase in prostate cancers  
JOURNAL Patent: WO 0227324-A 3 04-APR-2002;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES  
Location/Qualifiers  
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1..1146  
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1..>1146  
/note="unnamed protein product";  
/codon\_start=1  
/protein\_id="CAD48643.1"  
/db\_xref="GI:23342547"  
/translation="MALQGSVVELSGIAPGFCAMVLADFGARVVRDPSRYDVS  
RLGRKSLVLDLQKPGAAVRLCKRSVLLLEPFRGVMKQLQGLPEILORENPLR  
IYARLSFGSGSFCRLAGHDINYLALSGVLSKIGRSNGENPYAPINLLADPAGGLMC  
ALYKLMALFDRTRTGQVQIDANNVEGTAYLSLFLWTKQSSLWEAPRQNMLDGAP  
FYTYRTADGEFMAVGAIEPQFYELLIKGLKSDLEPNQMSDDWPEMKKKFADVFA  
KKTAKWCQIFDGDACVTPVLTPEEVVHHDKNKGESFTISEBQDVSPPAPLLNT  
PAIPSPKRPDPFIEGTEILBEFGFSREIYQLNSDKIIESNKYKASL"

ORIGIN

Query Match 100.0%; Score 1146; DB 6; Length 1146;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCACTGCAGGCATCTCGTCTGAGCTGTCGGCCCTGGCCCGCCCGCTTCTGT 60  
|||||  
Db 1 ATGGCACTGCAGGCATCTCGTCTGAGCTGTCGGCCCTGGCCCGCCCGCTTCTGT 60  
|||||



|            |  |  |                            |
|------------|--|--|----------------------------|
| Db         | 666  | TCGAGTCTGTGGGAGACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTTCTAT    | 725                        |
| Qy         | 661  | ACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC    | 720                        |
| Db         | 726  | ACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC    | 785                        |
| Qy         | 721  | TACGAGCTGTGATCAAGAGCTTGGACTAAAGTCTGATGACTTCCCAATCAGATGAGC    | 780                        |
| Db         | 786  | TACGAGCTGTGATCAAGAGCTTGGACTAAAGTCTGATGACTTCCCAATCAGATGAGC    | 845                        |
| Qy         | 781  | ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAAAGAACGAGAG    | 840                        |
| Db         | 846  | ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAAAGAACGAGAG    | 905                        |
| Qy         | 841  | GCAGAGTGGTGTCAAAATCTTTGACCGCACAGATGCTGTGACTTCCGGTTCTGACTTTT  | 900                        |
| Db         | 906  | GCAGAGTGGTGTCAAAATCTTTGACCGCACAGATGCTGTGACTTCCGGTTCTGACTTTT  | 965                        |
| Qy         | 901  | GAGGAGTGTTCATCATGATCACAACAAAGGAAACCGGGCTGTTTATCACAAGTGAAG    | 960                        |
| Db         | 966  | GAGGAGTGTTCATCATGATCACAACAAAGGAAACCGGGCTGTTTATCACAAGTGAAG    | 1025                       |
| Qy         | 961  | CAGGAGTGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC   | 1020                       |
| Db         | 1026   | CAGGAGTGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC   | 1085                       |
| Qy         | 1021   | AAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTACG | 1080                       |
| Db         | 1086   | AAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTACG | 1145                       |
| Qy         | 1081   | CGGAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAAGCT            | 1140                       |
| Db         | 1146   | CGGAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAAGCT            | 1205                       |
| Qy         | 1141   | AGTCTC 1146  |                            |
| Db         | 1206   | AGTCTC 1211  |                            |
| RESULT 3   |  |  |                            |
| AX497161   |  |  |                            |
| LOCUS      | AX497161   | 2005 bp  | DNA linear PAT 26-SEP-2002 |
| DEFINITION | Sequence 10 from Patent WO0227324.                     |  |                            |
| ACCESSION  | AX497161   |  |                            |
| VERSION    | AX497161.1   | GI:23342554  |                            |
| KEYWORDS   |  |  |                            |
| SOURCE     | Homo sapiens (human)                                   |  |                            |
| ORGANISM   | Homo sapiens   |  |                            |
| REFERENCE  | 1  |  |                            |
| AUTHORS    | Richardson, J.   |  |                            |
| TITLE      | Alpha-methylacyl-coa racemase in prostate cancers      |  |                            |
| JOURNAL    | Patent: WO 0227324-A 10 04-APR-2002;                   |  |                            |
| FEATURES   | Millennium Pharmaceuticals, Inc. (US)                  |  |                            |
| source     | Location/Qualifiers                                    |  |                            |
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| Qy | 61   | GCTATGCTCTGCTGACTTCCGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCGCG    | 120  |
| Db | 126  | GCTATGCTCTGCTGACTTCCGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCGCG    | 185  |
| Qy | 121  | TACGACGTGAGCCGCTTTGGCGCGCAAGCGCTCGTGTAGTGTGAGCTTGAAGCAGCG    | 180  |
| Db | 186  | TACGACGTGAGCCGCTTTGGCGCGCAAGCGCTCGTGTAGTGTGAGCTTGAAGCAGCG    | 245  |
| Qy | 181  | CGGGAGCGCGCTGTGCGCGCTGTGTCAAGCGGTGCGATGTGCTGTGAGCCCTTC       | 240  |
| Db | 246  | CGGGAGCGCGCTGTGCGCGCTGTGTCAAGCGGTGCGATGTGCTGTGAGCCCTTC       | 305  |
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| Db | 306  | CGCCCGGTGTATGAGGAACTCCAGCTGGCGCCAGAGATTTCTGCAGCGGAAATCCA     | 365  |
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| Db | 366  | AGGCTTATTTATGCCAGCGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCGGTTAGCT  | 425  |
| Qy | 361  | GGCCACGATATCAACTATTTGGCTTTGTACAGTGTCTCTCAAAATTTGGCAGAGTGGT   | 420  |
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| Db | 546  | GCATGGGCAATTAATAGGCTCTTTTGGCCGACACGCACTGGCAAGGGTCAAGTCAAT    | 605  |
| Qy | 541  | GATGCAATATGTTGGAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAATCTCAGAAA   | 600  |
| Db | 606  | GATGCAATATGTTGGAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAATCTCAGAAA   | 665  |
| Qy | 601  | TCGAGTCTGTGGAGGACCTCGAGGACAGACATGTTGGATGTTGGAGCACCTTCTAT     | 660  |
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| Db | 726  | ACGACTTACAGGACAGCAGATGGGAAATTCATGCTGTGGAGCAATAGAACCCAGTTC    | 785  |
| Qy | 721  | TACGAGTGTGATCAAAAGGACTTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC | 780  |
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RESULT 4
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LOCUS AF158378
DEFINITION Homo sapiens alpha-methylacyl-CoA racemase (RM) mRNA, complete cds.
ACCESSION AF158378
VERSION AF158378.1 GI:6653127
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2005)
AUTHORS Ferdinandusse, S., Denis, S., Clayton, P.T., Graham, A., Rees, J.E.,
Allen, J.T., McLean, B.N., Brown, A.Y., Vreken, P., Waterham, H.R. and
Wanders, R.J.
MUTATIONS in the gene encoding peroxisomal alpha-methylacyl-CoA
racemase cause adult-onset sensory motor neuropathy
Nat. Genet. 24 (2), 188-191 (2000)
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PUBMED 1065068
REFERENCE 2 (bases 1 to 2005)
AUTHORS Ferdinandusse, S., Denis, S. and Wanders, R.J.A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1999) Clinical Chemistry, Academic Medical
Center, Meibergdreef 9, Amsterdam 1105 AZ, The Netherlands
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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AX497155 2069 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 4 from Patent WO0227324.  
ACCESSION AX497155  
VERSION AX497155.1 GI:23342548  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Richardson, J.  
TITLE Alpha-methylacyl-coa racemase in prostate cancers  
JOURNAL Patent: WO 0227324-A 4 04-APR-2002;  
Millennium Pharmaceuticals, Inc. (US)  
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Best Local Similarity 100.0%; Pred. No. 0;  
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DB 270 CCGGAGCCCGCTGCTGGCGGCTCTGTGCAAGCGGTGGATGTCTGCTGGAGCCCTTC 329

QY 241 CGCCCGGTGTCTATGAGAGAACTCCAGCTGGGCCCGAGAGATTTCTGACGGGAGAAATCA 300  
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RESULT 6  
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LOCUS AX497157 3654 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 6 from Patent WO0227324.  
ACCESSION AX497157  
VERSION AX497157.1 GI:23342550  
KEYWORDS Homo sapiens (human)  
SOURCE

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| ORGANISM                   | Homo sapiens  |
| REFERENCE                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |
| AUTHORS                    | 1 Richardson, J.  |
| TITLE                      | Alpha-methylacyl-coa racemase in prostate cancers   |
| JOURNAL                    | Patent: WO 0227324-A 6 04-APR-2002; Millennium Pharmaceuticals, Inc. (US)   |
| FEATURES                   | Location/Qualifiers   |
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| ORIGIN                     |   |
| Query Match                | 98.8%; Score 1132; DB 6; Length 3654;   |
| Best Local Similarity      | 100.0%; Pred. No. 0;  |
| Matches 1132; Conservative | 0; Mismatches 0; Indels 0; Gaps 0;  |
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| Db         | 870 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATATTGCAAAAGAACGCAAG 929   |
| QY         | 841 GCAGAGTGGTCAAAATCTTTTGACGGCACAGATGCCTGTGACTCCGGTCTCAGCTTTT 900   |
| Db         | 930 GCAGAGTGGTCAAAATCTTTTGACGGCACAGATGCCTGTGACTCCGGTCTCAGCTTTT 989   |
| QY         | 901 GAGGAGTGTCTCATCATGATCAACAAGAAACGGGGCTCGTTTATCACCAGTGAGGAG 960  |
| Db         | 990 GAGGAGTGTCTCATCATGATCAACAAGAAACGGGGCTCGTTTATCACCAGTGAGGAG 1049   |
| QY         | 961 CAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACCCAGCACTCCCTTCTTTC 1020  |
| Db         | 1050 CAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACCCAGCACTCCCTTCTTTC 1109   |
| QY         | 1021 AAAAGGATCCTTTCATAGGAAACACACTGAGGAGATCTTGAAGATTTGGATTTCAGC 1080  |
| Db         | 1110 AAAAGGATCCTTTCATAGGAAACACACTGAGGAGATCTTGAAGATTTGGATTTCAGC 1169  |
| QY         | 1081 CGGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGG 1132  |
| Db         | 1170 CGGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGG 1221  |
| RESULT 7   |  |
| BD242020   | 1621 bp DNA linear PAT 17-JUL-2003   |
| LOCUS      | Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.                                      |
| DEFINITION | BD242020   |
| ACCESSION  | BD242020   |
| VERSION    | BD242020.1 GI:33051790   |
| KEYWORDS   | JP 2002520054-A/107.   |
| SOURCE     | Homo sapiens (human)   |
| ORGANISM   | Homo sapiens   |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| AUTHORS    | Dillon, D.C., Harlocker, S.L., Yugiu, J., Xu, J. and Mitcham, J.L.   |
| TITLE      | Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use                                       |
| JOURNAL    | Patent: JP 2002520054-A 107 09-JUL-2002;   |
| COMMENT    | CORIXA CORP  |
|            | OS Homo sapiens (human)  |
|            | PN JP 2002520054-A/107   |
|            | PD 09-JUL-2002   |
|            | PF 14-JUL-1999 JP 2000560247   |
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|            | 23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR   |
|            | 15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR   |
|            | 09-APR-1999 US 09/288946   |
|            | PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANGL YUQIU, PI   |
|            | JIANGCHUN XU,  |
|            | PI JENNIFER LYNN MITCHAM   |
|            | PC C12N15/09,A61K38/00,A61K39/395,C07K14/47,C07K16/30,   |
|            | PC C12N5/10,   |
|            | PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,   |
|            | PC A61K37/02,  |
|            | PC C12N5/00  |
|            | CC Compounds for immunotherapy and diagnosis of prostate cancer  |
|            | CC and methods   |
|            | CC for their use   |

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PH Key Location/Qualifiers
FT source 1. .1621 /organism='Homo sapiens (human)'.
FT Location/Qualifiers
FEATURES
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ORIGIN
Query Match 93.4%; Score 1070; DB 6; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCGGGCTGCGCCCGGCGCTTCTGTGCTATGCTCTGGCTGACTTCGGGG 85
DB 30 TGGAGCTGTCGGGCTGCGCCCGGCGCTTCTGTGCTATGCTCTGGCTGACTTCGGGG 89
QY 86 CGCGTGTGTAGCGTGGACCGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 145
DB 90 CGCGTGTGTAGCGTGGACCGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 149
QY 146 GCAAGCGCTCGCTAGTGTGGAACCTGAAGCAGCGCGGGAGCGCGCTGCGCGCTC 205
DB 150 GCAAGCGCTCGCTAGTGTGGAACCTGAAGCAGCGCGGGAGCGCGCTGCGCGCTC 209
QY 206 TGTCAAGCGCTCGGATGCTGTGAGCGCTTCCGCGCGGCTGTGAGAAACTCC 265
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DB 270 AGCTGGGCGGACAGATTCGACGCGGGAATCCAGGCTTATTTATGCGAGCTGAGTG 329
QY 326 GATTTGGCGAGTCAGGAAGCTTCTCGCGGTAGCTGGCCACGATATCAACTATTTGGGTT 385
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QY 386 TGTCAAGCTGTTCTCAAAAATGGCAGAGTGGTGAATCCGCTATGCCCGCTGAATC 445
DB 390 TGTCAAGCTGTTCTCAAAAATGGCAGAGTGGTGAATCCGCTATGCCCGCTGAATC 449
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QY 566 CATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 625
DB 570 CATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 629
QY 626 GACAGAACATGTTGATGTGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG 685
DB 630 GACAGAACATGTTGATGTGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG 689
QY 686 AATTTCATGCTGTGAGCAATAGAACCCCGCTTCTACGAGCTGTGATCAAGGACTTG 745
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QY 746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATTTGGCCAGAAATGAAGA 805
DB 750 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATTTGGCCAGAAATGAAGA 809
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DB 810 AGAAGTTGACAGATGTAATTTGCAAAAGACGAGGAGTGGTGTCAAATCTTTTGAAG 869
QY 866 GCACAGATGCCGTGCTGCTCGGCTTCGACTTTTGAAGGAGTGTTCATCATGATATCA 925
DB 870 GCACAGATGCCGTGCTGCTCGGCTTCGACTTTTGAAGGAGTGTTCATCATGATATCA 929
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QY 926 ACAAGGAACGGGGCTCGTTTATCACCAGTGAAGGACGAGAGCTGAGCCCCCGCCCTGAC 985
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QY 986 CTCTGCTGTAAACACACCCAGCCATCCCTTCTTTTCAAAAGGAGTCTTTTCATAGGAGAC 1045
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DB 1110 CAGATAAATCATTTGAAAAGTAAATAGGTAAAGCTAGTCTC 1150

RESULT 8
AR237203
LOCUS 1621 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 107 from patent US 6465611.
ACCESSION AR237203
VERSION AR237203.1 GI:27281861
KEYWORDS
SOURCE Unknown.
ORGANISM Unclausified.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6465611-A 107 15-OCT-2002;
FEATURES Location/Qualifiers
source 1. .1621
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ORIGIN
Query Match 93.4%; Score 1070; DB 6; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCGGGCTGCGCCCGGCGCTTCTGTGCTATGCTCTGGCTGACTTCGGGG 85
DB 30 TGGAGCTGTCGGGCTGCGCCCGGCGCTTCTGTGCTATGCTCTGGCTGACTTCGGGG 89
QY 86 CGCGTGTGTAGCGTGGACCGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 145
DB 90 CGCGTGTGTAGCGTGGACCGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 149
QY 146 GCAAGCGCTCGCTAGTGTGGAACCTGAAGCAGCGCGGGAGCGCGCTGCGCGCTC 205
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Db 510 TTGACCGCACAGCAGCTGCAAGGTCAGGTCATTGATGCAAAATATGGTGAAGAACAG 569  
Qy 566 CATATTTAAGTCTCTTTCTGTGGAAACTCAGAAATCGAGTCGTGGGAAGCACTCGAG 625  
Db 570 CATATTTAAGTCTCTTTCTGTGGAAACTCAGAAATCGAGTCGTGGGAAGCACTCGAG 629  
Qy 626 GACAGAACATGTGGATGGAGACACCTTTCTATACGACTTACAGGACAGATGGG 685  
Db 630 GACAGAACATGTGGATGGAGACACCTTTCTATACGACTTACAGGACAGATGGG 689  
Qy 686 AATTCATGGCTGTGGAGCAATAGAACCCAGTTCTAGAGCTGCTGATCAAGGACTTG 745  
Db 690 AATTCATGGCTGTGGAGCAATAGAACCCAGTTCTAGAGCTGCTGATCAAGGACTTG 749  
Qy 746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 805  
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Qy 866 GCACAGATGCCGTGTGACTCGGTTCTGACTTTTGGAGAGTGTTCATCATGATCACA 925  
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RESULT 9  
AR278227  
LOCUS AR278227 1621 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 107 from patent US 6512094.  
ACCESSION AR278227  
VERSION AR278227.1 GI:29712473  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1621)  
XU,J., DILLON,D.C., MITCHAM,J.L., HARLOCKER,S.L., JIANG,Y.,  
KALOS,M.D., FANGER,G.R., RETTER,M.W., STOLK,J.A., DAY,C.H.,  
VEDVICK,T.S., CARTER,D., LI,S.X., WANG,A., SKEIKY,Y.A.W.,  
HEPLER,W.T. and HENDERSON,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6512094-A 107 28-JAN-2003;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 93.4%; Score 1070; DB 6; Length 1621;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 26 TGGAGCTGTCCGGCTCGCCCTGGCCCCCGGGCCCGTTCTGTGTATGTGCTCTGCTGACTTCGGGG 85  
Db 30 TGGAGCTGTCCGGCTCGCCCTGGCCCCCGGGCCCGTTCTGTGTATGTGCTCTGCTGACTTCGGGG 89  
Qy 86 CGCGTGTGGTACGCGTGGAGCCGGCCCGGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 145  
Db 90 CGCGTGTGGTACGCGTGGAGCCGGCCCGGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 149  
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Qy 566 CATATTTAAGTCTCTTTCTGTGGAAACTCAGAAATCGAGTCGTGGGAAGCACTCGAG 625  
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|    |      |  |      |
|----|------|--|------|
| Qy | 206  | TGTCAAGCGTTCGATGTCTGCTGGAGCCCTTCCGCGCGTGTCTATGAGAAACTCC      | 265  |
| Ds | 210  | TGTCAAGCGTTCGATGTCTGCTGGAGCCCTTCCGCGCGTGTCTATGAGAAACTCC      | 269  |
| Qy | 266  | AGCTGGGCCAGAGATCTTCAGAGGGGAAATCAAAGCTTATTTATGCCAGGCTGAGTG    | 325  |
| Ds | 270  | AGCTGGGCCAGAGATCTTCAGAGGGGAAATCAAAGCTTATTTATGCCAGGCTGAGTG    | 329  |
| Qy | 326  | GATTGGCCAGTCAGGAAGCTTCTCGCGGTAGCTGGCCAGCATCAACTATTTTGGCTT    | 385  |
| Ds | 330  | GATTGGCCAGTCAGGAAGCTTCTCGCGGTAGCTGGCCAGCATCAACTATTTTGGCTT    | 389  |
| Qy | 386  | TGTCAGGTGTTCTCTCAAAAATGGCAGAAAGTGTGAGAAATCCGTATGCCCGCTGAATC  | 445  |
| Ds | 390  | TGTCAGGTGTTCTCTCAAAAATGGCAGAAAGTGTGAGAAATCCGTATGCCCGCTGAATC  | 449  |
| Qy | 446  | TCCTGGCTGACTTGTCTGGTGGTGGCTTATGTGTGCACTGGGCATTTAATATGCTCTTT  | 505  |
| Ds | 450  | TCCTGGCTGACTTGTCTGGTGGTGGCTTATGTGTGCACTGGGCATTTAATATGCTCTTT  | 509  |
| Qy | 506  | TTGACCGCACAGCACTGGCAAGGTCAGGTCATTTGATGCAAAATATGTTGGAAGAACAG  | 565  |
| Ds | 510  | TTGACCGCACAGCACTGGCAAGGTCAGGTCATTTGATGCAAAATATGTTGGAAGAACAG  | 569  |
| Qy | 566  | CATATTTAAAGTCTCTTCTGTGAAACTCAGAAATCGAGTCTGTGGGAAGCACTCGAG    | 625  |
| Ds | 570  | CATATTTAAAGTCTCTTCTGTGAAACTCAGAAATCGAGTCTGTGGGAAGCACTCGAG    | 629  |
| Qy | 626  | GACAGAACATGTTGGATGGTGGAGCACTTCTATACGACTTACAGACAGCATGGGG      | 685  |
| Ds | 630  | GACAGAACATGTTGGATGGTGGAGCACTTCTATACGACTTACAGACAGCATGGGG      | 689  |
| Qy | 686  | AATTCATGGCTGTTGGAGCAATAGAACCCAGTCTTACGAGCTGCTGATCAAGAGACTTG  | 745  |
| Ds | 690  | AATTCATGGCTGTTGGAGCAATAGAACCCAGTCTTACGAGCTGCTGATCAAGAGACTTG  | 749  |
| Qy | 746  | GACTAAAGTCTGATGAATCTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA | 805  |
| Ds | 750  | GACTAAAGTCTGATGAATCTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA | 809  |
| Qy | 806  | AGAAAGTTGACAGATGATTTGCAAGAGCAAGGAGGAGTGGTGTCTTAATCTTTGACG    | 865  |
| Ds | 810  | AGAAAGTTGACAGATGATTTGCAAGAGCAAGGAGGAGTGGTGTCTTAATCTTTGACG    | 869  |
| Qy | 866  | GCACAGATGCTGTGACTCGGTTCTGACTTTTGTAGGAGGTTGTTTCATCATGATCACA   | 925  |
| Ds | 870  | GCACAGATGCTGTGACTCGGTTCTGACTTTTGTAGGAGGTTGTTTCATCATGATCACA   | 929  |
| Qy | 926  | ACAAGGAACGGGCTCGTTTATCACAGTGAGGAGCAGGAGCTGAGCCCCCGCTGCAC     | 985  |
| Ds | 930  | ACAAGGAACGGGCTCGTTTATCACAGTGAGGAGCAGGAGCTGAGCCCCCGCTGCAC     | 989  |
| Qy | 986  | CTCTGCTTTAAACACCCAGCCATCCCTTTCTTTCAAAGGGATCCTTTTCATAGGAAAC   | 1045 |
| Ds | 990  | CTCTGCTTTAAACACCCAGCCATCCCTTTCTTTCAAAGGGATCCTTTTCATAGGAAAC   | 1049 |
| Qy | 1046 | ACACTGAGGAGTACTTGAAGATTTGCAATTCAGCCGCGAGAGATTTATCAGCTTAACT   | 1105 |
| Ds | 1050 | ACACTGAGGAGTACTTGAAGATTTGCAATTCAGCCGCGAGAGATTTATCAGCTTAACT   | 1109 |
| Qy | 1106 | CAGATAAAATCATTTGAAAGTAATAGGTAAAGCTAGTCTC                     | 1146 |
| Ds | 1110 | CAGATAAAATCATTTGAAAGTAATAGGTAAAGCTAGTCTC                     | 1150 |

RESULT 12  
AR392324  
LOCUS AR392324 1621 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 107 from patent US 6613872.  
ACCESSION AR392324  
VERSION AR392324.1 GI:40116338  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1621)  
AUTHORS Xu, J. and Dillon, D. C.  
TITLE Compounds for immunotherapy of prostate cancer and methods for their use  
JOURNAL Patent: US 6613872-A 107 02-SEP-2003;  
FEATURES Location/Qualifiers  
source 1..1621  
/organism="unknown"  
/mol\_type="genomic DNA"

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| Query Match           | 93.4%        | Score 1070;  | DB 6;      | Length 1621; |
| Best Local Similarity | 99.9%        | Pred. No. 0;   |            |              |
| Matches 1120;         | Conservative | 0;   | Mismatches | 1;           |
| Indels                | 0;           | Gaps   | 0;         |              |
| Qy                    | 26           | TGAGAGCTGTCCGCGCTGGCCCCCGGGCCCGTTCGTGTGTATGTCCTGGCTGACATTCGGGG | 85         |              |
| Ds                    | 30           | TGAGAGCTGTCCGCGCTGGCCCCCGGGCCCGTTCGTGTGTATGTCCTGGCTGACATTCGGGG | 89         |              |
| Qy                    | 86           | CGCGTGTGGTACCGGTGGACCGCGCGGCTCCCGCTACGACCTGAGCGGCTTGGGCCGGG    | 145        |              |
| Ds                    | 90           | CGCGTGTGGTACCGGTGGACCGCGCGGCTCCCGCTACGACCTGAGCGGCTTGGGCCGGG    | 149        |              |
| Qy                    | 146          | GCAAGCGCTCGCTAGTGTCTGGACCTGAAAGCAGCGCGGGGAGCGCGCTGTGCGGGCTC    | 205        |              |
| Ds                    | 150          | GCAAGCGCTCGCTAGTGTCTGGACCTGAAAGCAGCGCGGGGAGCGCGCTGTGCGGGCTC    | 209        |              |
| Qy                    | 206          | TGTCAAAGCGGTCCGATGTCTGTCTGGAGCCCTTCCCGCGGGTGTATGAGAGAACTCC     | 265        |              |
| Ds                    | 210          | TGTCAAAGCGGTCCGATGTCTGTCTGGAGCCCTTCCCGCGGGTGTATGAGAGAACTCC     | 269        |              |
| Qy                    | 266          | AGCTGGGCCAGAGATTTCTGACGGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG    | 325        |              |
| Ds                    | 270          | AGCTGGGCCAGAGATTTCTGACGGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG    | 329        |              |
| Qy                    | 326          | GATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCTGGCCACGATATCAACTATTTTGGCTT   | 385        |              |
| Ds                    | 330          | GATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCTGGCCACGATATCAACTATTTTGGCTT   | 389        |              |
| Qy                    | 386          | TGTCAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGGTGAAGATCCGATATGCCCGCTGAATC | 445        |              |
| Ds                    | 390          | TGTCAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGGTGAAGATCCGATATGCCCGCTGAATC | 449        |              |
| Qy                    | 446          | TCCTGGCTGACTTGTCTGGTGGTGGCTTATGTGTGCACTGGGCAATTAATATGCTCTTT    | 505        |              |
| Ds                    | 450          | TCCTGGCTGACTTGTCTGGTGGTGGCTTATGTGTGCACTGGGCAATTAATATGCTCTTT    | 509        |              |
| Qy                    | 506          | TTGACCGCACAGCACTGGCAAGGTCAGGTCATTTGATGCAAAATATGTTGGAAGAACAG    | 565        |              |
| Ds                    | 510          | TTGACCGCACAGCACTGGCAAGGTCAGGTCATTTGATGCAAAATATGTTGGAAGAACAG    | 569        |              |
| Qy                    | 566          | CATATTTAAAGTCTCTTCTGTGAAAACTCAGAAATCGAGTCTGTGGAAAGCACTCGAG     | 625        |              |
| Ds                    | 570          | CATATTTAAAGTCTCTTCTGTGAAAACTCAGAAATCGAGTCTGTGGAAAGCACTCGAG     | 629        |              |
| Qy                    | 626          | GACAGAACATGTTGGATGGTGGAGCACTTCTATACGACTTACAGACAGCATGGGG        | 685        |              |
| Ds                    | 630          | GACAGAACATGTTGGATGGTGGAGCACTTCTATACGACTTACAGACAGCATGGGG        | 689        |              |
| Qy                    | 686          | AATTCATGGCTGTTGGAGCAATAGAACCCAGTCTTACGAGCTGCTGATCAAGAGACTTG    | 745        |              |
| Ds                    | 690          | AATTCATGGCTGTTGGAGCAATAGAACCCAGTCTTACGAGCTGCTGATCAAGAGACTTG    | 749        |              |
| Qy                    | 746          | GACTAAAGTCTGATGAATCTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA   | 805        |              |
| Ds                    | 750          | GACTAAAGTCTGATGAATCTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA   | 809        |              |
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| Ds                    | 810          | AGAAAGTTGACAGATGATTTGCAAGAGCAAGGAGGAGTGGTGTCTTAATCTTTGACG      | 869        |              |
| Qy                    | 866          | GCACAGATGCTGTGACTCGGTTCTGACTTTTGTAGGAGGTTGTTTCATCATGATCACA     | 925        |              |
| Ds                    | 870          | GCACAGATGCTGTGACTCGGTTCTGACTTTTGTAGGAGGTTGTTTCATCATGATCACA     | 929        |              |
| Qy                    | 926          | ACAAGGAACGGGCTCGTTTATCACAGTGAGGAGCAGGAGCTGAGCCCCCGCTGCAC       | 985        |              |
| Ds                    | 930          | ACAAGGAACGGGCTCGTTTATCACAGTGAGGAGCAGGAGCTGAGCCCCCGCTGCAC       | 989        |              |
| Qy                    | 986          | CTCTGCTTTAAACACCCAGCCATCCCTTTCTTTCAAAGGGATCCTTTTCATAGGAAAC     | 1045       |              |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Patent No. US20020123081A1  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE  
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS  
; FILE REFERENCE: 07334-312001  
; CURRENT APPLICATION NUMBER: US/09/967,305  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/236,238  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 11  
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; NAME/KEY: CDS  
; LOCATION: (1)...(1146)  
US-09-967-305-3

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; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2005
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; US-09-967-305-1

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Best Local Similarity 100.0%; Pred. No. 0;
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## RESULT 3

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; Patent No. US20020123081A1  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE  
; FILE OF INVENTION: REFRATORY AND METASTATIC PROSTATE CANCERS  
; FILE REFERENCE: 07334-312001  
; CURRENT APPLICATION NUMBER: US/09/967,305  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/236,238  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 2005  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (66)...(1211)  
US-09-967-305-10

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Best Local Similarity 100.0%; Pred. No. 0;

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DB 66 ATGCGACTGAGGGCATCTCGGTCGTGGAGCTGTCCGGCTGCGCCCGGCGGCTTCTGT 125

QY 61 GCTATGGTCTCTGCTGACTTTCGGGGCGCGTGTGGTACGGGTGACCGGGCCCGCTCCCCG 120  
DB 126 GCTATGGTCTCTGCTGACTTTCGGGGCGCGTGTGGTACGGGTGACCGGGCCCGCTCCCCG 185  
QY 121 TAGAGCTGAGCGCGCTTGGGCGGAGCGCTCGCTAGTGTGACCTTGAAGCAGCG 180  
DB 186 TAGAGCTGAGCGCGCTTGGGCGGAGCGCTCGCTAGTGTGACCTTGAAGCAGCG 245  
QY 181 CGGGGAGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGCTGCTGGAGCCCTTC 240  
DB 246 CGGGGAGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGCTGCTGGAGCCCTTC 305  
QY 241 CGCGCGGTGTCATGAGAGAACTTCAGCTGGGCGGAGAGATTCGACGCGGAGAAATCCA 300  
DB 306 CGCGCGGTGTCATGAGAGAACTTCAGCTGGGCGGAGAGATTCGACGCGGAGAAATCCA 365  
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360  
DB 366 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 425  
QY 361 GCGCACGATATCAAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGCGAAGTGGT 420  
DB 426 GCGCACGATATCAAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGCGAAGTGGT 485  
QY 421 GAGAATCCGATGCGCCCGCTGAATCTCTGGCTGAACTTTGCTGGTGGTGGTCTTATGTGT 480  
DB 486 GAGAATCCGATGCGCCCGCTGAATCTCTGGCTGAACTTTGCTGGTGGTGGTCTTATGTGT 545  
QY 481 GCACCTGGGATTAATATGCTCTTTTGACCGGACACGACCTGCGGAGGTCAGTTCATT 540  
DB 546 GCACCTGGGATTAATATGCTCTTTTGACCGGACACGACCTGCGGAGGTCAGTTCATT 605  
QY 541 GATGCAAAATATGCTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGAATACTCAGAAA 600  
DB 606 GATGCAAAATATGCTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGAATACTCAGAAA 665  
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT 660  
DB 666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT 725  
QY 661 ACAGCTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTTC 720  
DB 726 ACAGCTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTTC 785  
QY 721 TAGAGCTGCTGATCAAGGACCTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780  
DB 786 TAGAGCTGCTGATCAAGGACCTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 845  
QY 781 ATGATGATTTGGCCAGAAATCAAGAACTTTGACAGATCTATTTGCAAGAAAGCAAG 840  
DB 846 ATGATGATTTGGCCAGAAATCAAGAACTTTGACAGATCTATTTGCAAGAAAGCAAG 905  
QY 841 GCAGAGTGGTCTCAAAATCTTTTGACGACACAGATGCTGTTGACCTCCGGTTCTGACTTTT 900  
DB 906 GCAGAGTGGTCTCAAAATCTTTTGACGACACAGATGCTGTTGACCTCCGGTTCTGACTTTT 965  
QY 901 GAGAGGTTGTTTCAATCATGATCAACAAGAAACGGGGCTCGTTTATCAACAGTGGAG 960  
DB 966 GAGAGGTTGTTTCAATCATGATCAACAAGAAACGGGGCTCGTTTATCAACAGTGGAG 1025  
QY 961 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCCGCATCCCTTCTTTC 1020  
DB 1026 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCCGCATCCCTTCTTTC 1085  
QY 1021 AAAAGGATCTTTTATAGAGAAACACACTGAGGAGATCTTGAAGAAATTTGATTTCAGC 1080  
DB 1086 AAAAGGATCTTTTATAGAGAAACACACTGAGGAGATCTTGAAGAAATTTGATTTCAGC 1145  
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAATCAATGAAAGTAAAGTAAAGCT 1140  
DB 1146 CGCGAAGAGATTATCAGCTTAACTCAGATAAATCAATGAAAGTAAAGTAAAGCT 1205



QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCGG 180  
DB 186 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCGG 245  
QY 181 CGGGAGCGCGGCTGCTGGCGGCTGTGTGAAGCGGTCGATGCTGTGAGCCCTTC 240  
DB 246 CGGGAGCGCGGCTGCTGGCGGCTGTGTGAAGCGGTCGATGCTGTGAGCCCTTC 305  
QY 241 CGCGCGGTGTATGAGGAACTCCAGCTGGGCCAGAGATTTCTGACGCGGAAATCCA 300  
DB 306 CGCGCGGTGTATGAGGAACTCCAGCTGGGCCAGAGATTTCTGACGCGGAAATCCA 365  
QY 301 AGGCTTATTTATGACGCTGAGTGGATTTGGCCAGTCAGAACTTCTGCGGTAGCT 360  
DB 366 AGGCTTATTTATGACGCTGAGTGGATTTGGCCAGTCAGAACTTCTGCGGTAGCT 425  
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAGTGT 420  
DB 426 GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAGTGT 485  
QY 421 GAGAACTCGTATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTATGCT 480  
DB 486 GAGAACTCGTATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTATGCT 545  
QY 481 GCACCTGGCATATTAATGGCTCTTTTGAACGCAACGCTGAGGAGGTCAGGTCAAT 540  
DB 546 GCACCTGGCATATTAATGGCTCTTTTGAACGCAACGCTGAGGAGGTCAGGTCAAT 605  
QY 541 GATCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTCGAAACTCAGAA 600  
DB 606 GATCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTCGAAACTCAGAA 665  
QY 601 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTTTGATGTTGGATGGTGAGCACCTTCTAT 660  
DB 666 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTTTGATGTTGGATGGTGAGCACCTTCTAT 725  
QY 661 ACAGCTTACAGGACAGCAGATGGGAATTCATGCTGTGAGCAATPAGAACCCAGTTC 720  
DB 726 ACAGCTTACAGGACAGCAGATGGGAATTCATGCTGTGAGCAATPAGAACCCAGTTC 785  
QY 721 TACGAGTGTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAC 780  
DB 786 TACGAGTGTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAC 845  
QY 781 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAAAGAACGCAAG 840  
DB 846 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAAAGAACGCAAG 905  
QY 841 GCAGAGTGTGTTCAAACTTTTGAACGACAGATGCTGTGAGCTCCGGTTCTGACTTTT 900  
DB 906 GCAGAGTGTGTTCAAACTTTTGAACGACAGATGCTGTGAGCTCCGGTTCTGACTTTT 965  
QY 901 GAGGAGTGTGTTCAATCATGATCAACAAGGAACGCGGCTCGTTTATCAACAGTGGAG 960  
DB 966 GAGGAGTGTGTTCAATCATGATCAACAAGGAACGCGGCTCGTTTATCAACAGTGGAG 1025  
QY 961 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACCCCGACCCCTCTTCTTC 1020  
DB 1026 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACCCCGACCCCTCTTCTTC 1085  
QY 1021 AAAAGGGATCCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1080  
DB 1086 AAAAGGGATCCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1145  
QY 1081 CGGGAAGATTTATGAGTTAACTCAGATAAATCAATTGAAGTAAATAGGTAAGT 1140  
DB 1146 CGGGAAGATTTATGAGTTAACTCAGATAAATCAATTGAAGTAAATAGGTAAGT 1205  
QY 1141 AGTCTC 1146  
DB 1206 AGTCTC 1211

RESULT 6  
US-09-967-305-4  
; Sequence 4, Application US/09967305  
; Patent No. US20020123081A1  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE  
; FILE REFERENCE: 07334-312001  
; CURRENT APPLICATION NUMBER: US/09/967,305  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/236,238  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (90)...(1235)  
US-09-967-305-4

Query Match 100.0%; Score 1146; DB 9; Length 2069;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGACTGACGGGCATCTCGTCTGTGAGCTGTCTCGGCTGTGCGCCCTGCGGCCCGGCGCTTCGT 60  
DB 90 ATGCGACTGACGGGCATCTCGTCTGTGAGCTGTCTCGGCTGTGCGGCCCGGCGCTTCGT 149  
QY 61 GCTATGCTCTGCTGACTTTCGGGGCGGCTGTGTGACGCTGTGACCGCGGCGGCTCCGC 120  
DB 150 GCTATGCTCTGCTGACTTTCGGGGCGGCTGTGTGACGCTGTGACCGCGGCGGCTCCGC 209  
QY 121 TAGGACGTGACCGCTTGGGCGGGCAAGCGCTCGCTAGTGTGAGACCTTGAAGCAGCG 180  
DB 210 TAGGACGTGACCGCTTGGGCGGGCAAGCGCTCGCTAGTGTGAGACCTTGAAGCAGCG 269  
QY 181 CGGGAGCGCCGCTGTGCTGGCGCTGTGTGCAAGCGGTCGATGCTGTGAGCCCTTC 240  
DB 270 CGGGAGCGCCGCTGTGCTGGCGCTGTGTGCAAGCGGTCGATGCTGTGAGCCCTTC 329  
QY 241 CGCGCGGCTGTATGAGAACTTCCAGCTGGGCCAGAGATTTCTGACGCGGAAATCCA 300  
DB 330 CGCGCGGCTGTATGAGAACTTCCAGCTGGGCCAGAGATTTCTGACGCGGAAATCCA 389  
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTCCGCTTAGCT 360  
DB 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTCCGCTTAGCT 449  
QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGT 420  
DB 450 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAGTGT 509  
QY 421 GAGAACTCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGCT 480  
DB 510 GAGAACTCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGCT 569  
QY 481 GCACCTGGCATATTAATGGCTCTTTTGAACGACACGCTGCGAAGGTCAGGTCAAT 540  
DB 570 GCACCTGGCATATTAATGGCTCTTTTGAACGACACGCTGCGAAGGTCAGGTCAAT 629  
QY 541 GATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCAGAAA 600  
DB 630 GATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCAGAAA 689  
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 660  
DB 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 749

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QY 661 ACAGCTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 720
Db 750 ACAGCTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 809
QY 721 TAGGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 810 TAGGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 869
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACAGATGTATTTGCAAGAAGACGAAG 840
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACAGATGTATTTGCAAGAAGACGAAG 929
QY 841 GCAGAGTGGTCAAAATCTTTGACGGACAGATGCTGTGATCCTCGGTCTGACTTTT 900
Db 930 GCAGAGTGGTCAAAATCTTTGACGGACAGATGCTGTGATCCTCGGTCTGACTTTT 989
QY 901 GAGGAGTGTTCATCATGATACAAACAGGAACGGGCTCGTTTATACCAAGTGAAGGAG 960
Db 990 GAGGAGTGTTCATCATGATACAAACAGGAACGGGCTCGTTTATACCAAGTGAAGGAG 1049
QY 961 CAGGAGCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1050 CAGGAGCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1109
QY 1021 AAAAGGATCTTTTCATAGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1080
Db 1110 AAAAGGATCTTTTCATAGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1169
QY 1081 CGCGAGAGATTTATCAGCTTACTCAGATAAAATCATTTGAAAGTAAAGT 1140
Db 1170 CGCGAGAGATTTATCAGCTTACTCAGATAAAATCATTTGAAAGTAAAGT 1229
QY 1141 AGTCTC 1146
Db 1230 AGTCTC 1235

RESULT 7
US-10-205-823-17
; Publication 17, Application US/10205823
; General Information:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
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; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-17

Query Match 100.0%; Score 1146; DB 15; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCANCTCGGTCTGTGAGCTGTCCGGCTGGCCCCCGGGCCGGTCTGT 60
Db 90 ATGGCACTGCAGGGCANCTCGGTCTGTGAGCTGTCCGGCTGGCCCCCGGGCCGGTCTGT 149
QY 61 GCTATGCTCTCGCTGACTTTCGGGGCGCGTGTGAGCTGTGACGGCGCGGCTCCCGCTCCCGC 120
Db 150 GCTATGCTCTCGCTGACTTTCGGGGCGCGTGTGAGCTGTGACGGCGCGGCTCCCGCTCCCGC 209
QY 121 TACGACGTGAGCGCGCTTGGCGCGGGGCAAGCGCTCGCTAGTCTGTGACCTGAAGCAGCGG 180
Db 210 TACGACGTGAGCGCGCTTGGCGCGGGGCAAGCGCTCGCTAGTCTGTGACCTGAAGCAGCGG 269
QY 181 CGGGAGAGCGCGCTGTGCGGGCTGTGTCGAAGCGGTCCGATGTGCTGTGAGCCCTTC 240
Db 270 CGGGAGAGCGCGCTGTGCGGGCTGTGTCGAAGCGGTCCGATGTGCTGTGAGCCCTTC 329
QY 241 CGCGCGGCTGTCTATGAGGAACTCCAGCTGGGCGGCAAGATCTCGCAGCGGGAATCCA 300
Db 330 CGCGCGGCTGTCTATGAGGAACTCCAGCTGGGCGGCAAGATCTCGCAGCGGGAATCCA 389
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 449
QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 420
Db 450 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 509
QY 421 GAGATCCGTATGCCCGCTGAATCTCCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 480
Db 510 GAGATCCGTATGCCCGCTGAATCTCCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 569
QY 481 GCACCTGGCATTTATATGCTCTTTTGGACCGCACACGCACTGGCAAGGCTCAGGTCATT 540
Db 570 GCACCTGGCATTTATATGCTCTTTTGGACCGCACACGCACTGGCAAGGCTCAGGTCATT 629
QY 541 GATGCAAAATATGTTGGAAGAAACAGCATATTTAAGTCTTTTCTGTGGAATACTCAGAAA 600
Db 630 GATGCAAAATATGTTGGAAGAAACAGCATATTTAAGTCTTTTCTGTGGAATACTCAGAAA 689
QY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGACATCTTGATGCTGGAGCACCTTTCTAT 660
Db 690 TCGAGTCTGTGGGAAGCACTCGAGGACAGACATCTTGATGCTGGAGCACCTTTCTAT 749
QY 661 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 720
Db 750 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 809
QY 721 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 869
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACAGATGTATTTGCAAGAAGACGAAG 840
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACAGATGTATTTGCAAGAAGACGAAG 929
QY 841 GCAGAGTGGTCAAAATCTTTGACGGACAGATGCTGTGATCCTCGGTCTGACTTTT 900
Db 930 GCAGAGTGGTCAAAATCTTTGACGGACAGATGCTGTGATCCTCGGTCTGACTTTT 989
QY 901 GAGGAGTGTTCATCATGATACAAACAGGAACGGGCTCGTTTATACCAAGTGAAGGAG 960
Db 990 GAGGAGTGTTCATCATGATACAAACAGGAACGGGCTCGTTTATACCAAGTGAAGGAG 1049
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Qy 961 CAGGACGTGAGCCCGCCCTGACCTCTGCTGTAAACACACCCAGCCATCCCTTCTTTC 1020  
 Db 1050 CAGGACGTGAGCCCGCCCTGACCTCTGCTGTAAACACACCCAGCCATCCCTTCTTTC 1109  
 Qy 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1080  
 Db 1110 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1169  
 Qy 1081 CGGAAAGAGATTATCAGCTTAACTCAGATAAAATCAATGAAAGTAAAGGTTAAAGCT 1140  
 Db 1170 CGGAAAGAGATTATCAGCTTAACTCAGATAAAATCAATGAAAGTAAAGGTTAAAGCT 1229  
 Qy 1141 AGTCTC 1146  
 Db 1230 AGTCTC 1235

RESULT 8

US-10-205-823-25  
 ; Sequence 25, Application US/10205823  
 ; Publication No. US20030108963A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlegel, Robert  
 ; APPLICANT: Monahan, John E.  
 ; APPLICANT: Endege, Wilson O.  
 ; APPLICANT: Gannavarapu, Manjula  
 ; APPLICANT: Gorbacheva, Bella  
 ; APPLICANT: Hoersch, Sebastian  
 ; APPLICANT: Kamatkar, Shubhangi  
 ; APPLICANT: Wonsay, Angela M.  
 ; APPLICANT: Glatt, Karen  
 ; APPLICANT: Zhao, Xumei  
 ; APPLICANT: Anderson, Dustin  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
 ; FILE REFERENCE: MRI-044  
 ; CURRENT APPLICATION NUMBER: US/10/205,823  
 ; CURRENT FILING DATE: 2002-07-25  
 ; PRIOR APPLICATION NUMBER: 60/307,982  
 ; PRIOR FILING DATE: 2001-07-25  
 ; PRIOR APPLICATION NUMBER: 60/314,356  
 ; PRIOR FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/325,020  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: 60/341,746  
 ; PRIOR FILING DATE: 2001-12-12  
 ; PRIOR APPLICATION NUMBER: 60/362,158  
 ; PRIOR FILING DATE: 2002-03-05  
 ; NUMBER OF SEQ ID NOS: 455  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 25  
 ; LENGTH: 2069  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-205-823-25

Query Match 99.9%; Score 1144.4; DB 15; Length 2069;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 ATGSCACTGAGGGCATCTCGGTGTTGAGCTGTTCGGCTGGCCCGGGCCCGGTTCTGT 60  
 Db 90 ATGSCACTGAGGGCATCTCGGTGTTGAGCTGTTCGGCTGGCCCGGGCCCGGTTCTGT 149  
 Qy 61 GCTATGCTCTGCTGATCTTGGGGCGCGGTGTGTAGCGTGACCGGCGCGGCTCCCGC 120  
 Db 150 GCTATGCTCTGCTGATCTTGGGGCGCGGTGTGTAGCGTGACCGGCGCGGCTCCCGC 209  
 Qy 121 TACGACGTGAGCGCTTGGGGCGCGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCGC 180  
 Db 210 TACGACGTGAGCGCTTGGGGCGCGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCGC 269

RESULT 9

US-09-759-143-107  
 ; Sequence 107, Application US/09759143  
 ; Patent No. US2002002248A1

Qy 181 CGGGGAGCCCGCGTGTGCGCGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGAGCCCTTC 240  
 Db 270 CGGGGAGCCCGCGTGTGCGCGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGAGCCCTTC 329  
 Qy 241 CGCGCGGTGTCTATGAGAGAACTCCAGCTGGGCCAGAGATTTCTGACAGCGGGAATCCCA 300  
 Db 330 CGCGCGGTGTCTATGAGAGAACTCCAGCTGGGCCAGAGATTTCTGACAGCGGGAATCCCA 389  
 Qy 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTCCCGGTTAGCT 360  
 Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTCCCGGTTAGCT 449  
 Qy 361 GGGCAGATATCAACTATTTGGCTTTGTCTAGGTGTTCTCTCAAAAATTTGCGAGAGTGGT 420  
 Db 450 GGGCAGATATCAACTATTTGGCTTTGTCTAGGTGTTCTCTCAAAAATTTGCGAGAGTGGT 509  
 Qy 421 GAGAACTCGGTATGCCCGCTGAATCTCTCGCTGACTTTTCTGCTGTGCTGCTTATGTGT 480  
 Db 510 GAGAACTCGGTATGCCCGCTGAATCTCTCGCTGACTTTTCTGCTGTGCTGCTTATGTGT 569  
 Qy 481 GCACTGGGCATTATTAATGGCTCTTTTGTGACCGCACACGCACTGCAAGGCTCAGGTCAAT 540  
 Db 570 GCACTGGGCATTATTAATGGCTCTTTTGTGACCGCACACGCACTGCAAGGCTCAGGTCAAT 629  
 Qy 541 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCAGAAA 600  
 Db 630 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCAGAAA 689  
 Qy 601 TCCAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGAGGACACCTTCTAT 660  
 Db 690 TCCAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGAGGACACCTTCTAT 749  
 Qy 661 ACAGCTTACAGGACAGCATGCGGAATTCATGGCTGTTTGGAGCAATAGAACCCAGTTC 720  
 Db 750 ACAGCTTACAGGACAGCATGCGGAATTCATGGCTGTTTGGAGCAATAGAACCCAGTTC 809  
 Qy 721 TACAGCTGCTGATCAAAAGCACTTGGACTAAGTCTGATGAATCTTCCCAATCAGATGAGC 780  
 Db 810 TACAGCTGCTGATCAAAAGCACTTGGACTAAGTCTGATGAATCTTCCCAATCAGATGAGC 869  
 Qy 781 ATGAGTATTTGGCCAGAAATGAAGAGAGTTTGCAGATGATATTTGCAAAAGAGACGAAG 840  
 Db 870 ATGAGTATTTGGCCAGAAATGAAGAGAGTTTGCAGATGATATTTGCAAAAGAGACGAAG 929  
 Qy 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTTCGGTTCGTGACTTTT 900  
 Db 930 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTTCGGTTCGTGACTTTT 989  
 Qy 901 GAGGAGTTTTCATCATGATCAAAAGGAAACGGGGCTCGTTTATCAACAGTGAAGAG 960  
 Db 990 GAGGAGTTTTCATCATGATCAAAAGGAAACGGGGCTCGTTTATCAACAGTGAAGAG 1049  
 Qy 961 CAGGAGTGAAGCCCGCGCTGCACTCTGCTGTAAACACCCCGAGCCATCCCTTCTTTC 1020  
 Db 1050 CAGGAGTGAAGCCCGCGCTGCACTCTGCTGTAAACACCCCGAGCCATCCCTTCTTTC 1109  
 Qy 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGAGATTTCAGC 1080  
 Db 1110 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGAGATTTCAGC 1169  
 Qy 1081 CGGAAAGAGATTATCAGCTTAACTCAGATAAAATCAATGAAAGTAAAGGTTAAAGCT 1140  
 Db 1170 CGGAAAGAGATTATCAGCTTAACTCAGATAAAATCAATGAAAGTAAAGGTTAAAGCT 1229  
 Qy 1141 AGTCTC 1146  
 Db 1230 AGTCTC 1235

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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-759-143-107

Query Match      99.7%; Score 1142.8; DB 9; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGAGCGCATCTCGGTCTGGAGCTCTCGGCTGCGGCTGCGGCGGCGGCTCTGT 60
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DB 185 CGGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
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QY 361 GGCACAGATATCACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAGAGTGT 420
DB 365 GGCACAGATATCACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAGAGTGT 424
QY 421 GAGAACTCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 425 GAGAACTCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
QY 481 GCACCTGGCATTATAAGTCTTTTGGACCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 485 GCACCTGGCATTATAAGTCTTTTGGACCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 544
QY 541 GATGCNATATGGTGGAGGAACAGCATATTTAGTTCTTTCTGCTGGAACCTCAGAAA 600
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DB 545 GATCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTCTGTGAAAAAATCAGAAA 604
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DB 965 CAGGAGCTGAGCCCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
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DB 1025 AAAAGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC 1084
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAGGTAAAGCT 1140
DB 1085 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAGGTAAAGCT 1144
QY 1141 AGTCTC 1146
DB 1145 AGTCTC 1150
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RESULT 10
US-09-780-669-107
; Sequence 107, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 943  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-780-669-107

Query Match 99.7%; Score 1142.8; DB 9; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGCACCTGACGGGCACTCGGTCTGTGAGCTGTCCGGCTGTGGCCCGCCGGCCGCTTCTGT 60
DB 5 ATGCACCTGACGGGCACTCGGTCTGTGAGCTGTCCGGCTGTGGCCCGCCGGCCGCTTCTGT 64
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DB 65 GCTATGCTCTGCTGCTGCTTCCGGGCGCGTGTGCTAGCGTGGACCGCGCCGGCTCCCGC 124
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DB 365 GGCCACCATATCAACTATTTGGCTTCTCAGTGTCTCTCAAAAATGGCAGAGTGT 424
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DB 785 ATGATGATTTGGCCAGAAATCAGAAAGTTTTCAGATGTTTTCAGAAAGACCAAG 844
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DB 845 GCAGATGGTGTCAAATCTTTTACGCGACAGATGCTGTGACTCCGGTCTTCTGACTTTT 904
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QY 1081 CGCGAGAGATTTATCAGCTTAAGTCAAGATAAATCAATGAAAGTAAAGTAAAGT 1140
DB 1085 CGCGAGAGATTTATCAGCTTAAGTCAAGATAAATCAATGAAAGTAAAGTAAAGT 1144
QY 1141 AGTCTC 1146
DB 1145 AGTCTC 1150
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## RESULT 11

US-09-030-606-107

; Sequence 107, Application US/09030606

; Patent No. US20020081580A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Devin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS

; NUMBER OF SEQUENCES: 224

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED AND BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/030,606

; FILING DATE: 25-FEB-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.428C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 107:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1621 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; US-09-030-606-107

Query Match 99.7%; Score 1142.8; DB 9; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 5 ATGCACCTGACGGGCACTCGGTCTGTGAGCTGTCCGGCTGTGGCCCGCCGGCCGCTTCTGT 64
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Db 365 GGCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGCGAAGTGT 424  
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QY 1141 AGTCTC 1146  
Db 1145 AGTCTC 1150

RESULT 12  
US-09-822-827-107  
; Sequence 107, Application US/09822827  
; Patent No. US20020081680A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.534C1  
; CURRENT APPLICATION NUMBER: US/09/822,827  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; TYPE: DNA  
; LENGTH: 1621  
; ORGANISM: Homo sapien  
US-09-822-827-107

Query Match 99.7%; Score 1142.8; DB 9; Length 1621;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 125 TAGCAGCTGAGCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAGCAGCCG 184  
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QY 1081 CGGAGAGATTTATCAGCTTAACTCAGATAAATCACTGAGATAAAGTAAAGCT 1140  
Db 1085 CGGAGAGATTTATCAGCTTAACTCAGATAAATCACTGAGATAAAGTAAAGCT 1144  
QY 1141 AGTCTC 1146  
Db 1145 AGTCTC 1150

## RESULT 13

US-09-115-453-107  
; Sequence 107, Application US/09115453B  
; Patent No. US2002090372A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
; TITLE OF INVENTION: METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.427C4  
; CURRENT APPLICATION NUMBER: US/09/115,453B  
; CURRENT FILING DATE: 1998-07-14  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-115-453-107

Query Match 99.78; Score 1142.8; DB 9; Length 1621;  
Best Local Similarity 99.84; Pred. No. 0;  
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGGCACTGAGGGCATCTCGGTGCTGAGCTGTCCGGCTGCGCCCGGCGCCCGTCTCTGT 60  
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## RESULT 14

US-09-232-880-107  
; Sequence 107, Application US/09232880  
; Publication No. US20020182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn

QY 241 CGCCGGCTGCTCATGAGAAACTCCAGCTGGGCCCGCAGAGATTTCTGCAGCGGGAATCCCA 300  
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QY 421 GAGAACTCGTATGCCCGCTGAATCTCTCGCTGCTGACTTTCTGCTGCTGCTGCTGCTGCT 480  
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; CURRENT APPLICATION NUMBER: US/09/232,880  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; US-09-232-880-107

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; APPLICANT: Harlocker, Susan L.  
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; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
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; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.534C2  
; CURRENT APPLICATION NUMBER: US/09/895,793  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
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; ORGANISM: Homo sapien  
; US-09-895-793-107

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Db 1021 AAAAGGATCTTTTATAGAGAAACACACTGAGAGATATCTGAAGAAATTTGATTCAGC 1080
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATTAATCATTTGAAAGTAATGAAGTAAAGCT 1140
Db 1081 CGCGAAGAGATTATCAGCTTAACTCAGATTAATCATTTGAAAGTAATGAAGTAAAGCT 1140
QY 1141 AGTCTC 1146
Db 1141 AGTCTC 1146

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RESULT 2

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PCT-US02-24567-104
; Sequence 104, Application PC/TUS0224567
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Ruben, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: PCT/US02/24567
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 104
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24567-104

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Query Match 100.0%; Score 1146; DB 1; Length 2005;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-290;  
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCACTGAGGACATCTCGTCTGGAGCTGTCCGGCTGCGCCCGGGCCCGTCTGT 60
Db 66 ATGGCACTGAGGACATCTCGTCTGGAGCTGTCCGGCTGCGCCCGGGCCCGTCTGT 125
QY 61 GCTATGCTCTGCTGATCTTGGGGCGCGTGTGATGAGCGGCGGCGGCTCCCGC 120
Db 126 GCTATGCTCTGCTGATCTTGGGGCGCGTGTGATGAGCGGCGGCGGCTCCCGC 185
QY 121 TAGGAGTGTAGCCCGTGGCGGGGCAAGCGCTCGTGTGAGCACTGAAGAGCGCG 180

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RESULT 3  
 US-09-967-305-1

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Db 186 TAGACGTGAGCGCTTGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCGC 245
QY 181 CGGGAGAGCGCGCTGTGCGGGTCTGTGCAAGCGGTCCGATGTGTGTGAGCGCTTC 240
Db 246 CGGGAGAGCGCGCTGTGCGGGTCTGTGCAAGCGGTCCGATGTGTGTGAGCGCTTC 305
QY 241 CGCGCGGTGTCTATGAGAACTCCAGCTGGGCCCCAGAGATCTGCGAGCGGGAATCCA 300
Db 306 CGCGCGGTGTCTATGAGAACTCCAGCTGGGCCCCAGAGATCTGCGAGCGGGAATCCA 365
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTTCGCCGTTAGCT 360
Db 366 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTTCGCCGTTAGCT 425
QY 361 GGCACAGATATCAATATTTGGCTTTGTGTCAGGTGTTCTCTCAAAAATGGCAGAAAGTGGT 420
Db 426 GGCACAGATATCAATATTTGGCTTTGTGTCAGGTGTTCTCTCAAAAATGGCAGAAAGTGGT 485
QY 421 GAGATCCGATGCCCCCGCTGAATCTCTGCGCTGACTTTGCTGGTGGTGGCTTATGTCT 480
Db 486 GAGATCCGATGCCCCCGCTGAATCTCTGCGCTGACTTTGCTGGTGGTGGCTTATGTGT 545
QY 481 GCACCTGGGCTTATTAATGGCTCTTTTGACCGCACACGCTGGCAAGGCTCAGGTCAAT 540
Db 546 GCACCTGGGCTTATTAATGGCTCTTTTGACCGCACACGCTGGCAAGGCTCAGGTCAAT 605
QY 541 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTTCTTTCTGTGGAATACTCAGAAA 600
Db 606 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTTCTTTCTGTGGAATACTCAGAAA 665
QY 601 TCGAGTCTGTGGAGAGCACTCGAGGACAGACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db 666 TCGAGTCTGTGGAGAGCACTCGAGGACAGACATGTTGGATGGTGGAGCACCTTTCTAT 725
QY 661 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 726 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 785
QY 721 TAGGAGTCTGCTGATCAAAAGGACTTTGAGCTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 786 TAGGAGTCTGCTGATCAAAAGGACTTTGAGCTAAAGTCTGATGAATCTCCCAATCAGATGAGC 845
QY 781 ATGGATGATTGGCCAGAAATGAGAGAAAGTTTGCAGATGATATTTGCAAGAGAGAGCAAG 840
Db 846 ATGGATGATTGGCCAGAAATGAGAGAAAGTTTGCAGATGATATTTGCAAGAGAGAGCAAG 905
QY 841 GCAGAGTGTGTCAAAATCTTTGACCGCACAGATGCTGTGCTGACTCCGGTCTGACTTTT 900
Db 906 GCAGAGTGTGTCAAAATCTTTGACCGCACAGATGCTGTGCTGACTCCGGTCTGACTTTT 965
QY 901 GAGGAGTGTGTTTCATCATGATCAACAAGAGAAACGGGGCTCGTTTATCACCAGTGAAGG 960
Db 966 GAGGAGTGTGTTTCATCATGATCAACAAGAGAAACGGGGCTCGTTTATCACCAGTGAAGG 1025
QY 961 CAGGAGTGTAGCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGGCATCCCTTCTTTC 1020
Db 1026 CAGGAGTGTAGCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGGCATCCCTTCTTTC 1085
QY 1021 AAAAGGATCTTTTATAGAGAAACACACTGAGGAGATATCTGAAGAAATTTGATTCAGC 1080
Db 1086 AAAAGGATCTTTTATAGAGAAACACACTGAGGAGATATCTGAAGAAATTTGATTCAGC 1145
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATTAATCATTTGAAAGTAATGAAGTAAAGCT 1140
Db 1146 CGCGAAGAGATTATCAGCTTAACTCAGATTAATCATTTGAAAGTAATGAAGTAAAGCT 1205
QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

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; Sequence 1, Application US/09967305
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR FILING DATE: 2001-09-28
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-305-1

Query Match      100.0%; Score 1146; DB 44; Length 2005;
Best Local Similarity 100.0%; Pred. No. 4.7e-290;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCGGCGCCGGTCTCTGT 60
DB 66 ATGGCACTGAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCGGCGCCGGTCTCTGT 125
QY 61 GCTATGCTCTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGACCGCGCGCTCCCGC 120
DB 126 GCTATGCTCTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGACCGCGCGCTCCCGC 185
QY 121 TAGACGTGAGCGCTTGGCGCGGCGCAAGCGCTCCGTAGTGTGACCTGAGCAGCGCG 180
DB 186 TAGACGTGAGCGCTTGGCGCGGCGCAAGCGCTCCGTAGTGTGACCTGAGCAGCGCG 245
QY 181 CGGGAGCGCGCTGCTCGCGCGCTGTGCAAGCGGTGCGATGCTGTGAGAGCCCTTC 240
DB 246 CGGGAGCGCGCTGCTCGCGCGCTGTGCAAGCGGTGCGATGCTGTGAGAGCCCTTC 305
QY 241 CGCGCGGGTGTATGAGAAACTCCAGCTGGGCGCCAGAGATTTGAGCGGGGAAATCCA 300
DB 306 CGCGCGGGTGTATGAGAAACTCCAGCTGGGCGCCAGAGATTTGAGCGGGGAAATCCA 365
QY 301 AGGCTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAGAGACTTCTGCCGGTAGCT 360
DB 366 AGGCTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAGAGACTTCTGCCGGTAGCT 425
QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 420
DB 426 GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 485
QY 421 GAGAAATCCGATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGCGCTTATGTGT 480
DB 486 GAGAAATCCGATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGCGCTTATGTGT 545
QY 481 GCACCTGGCATTTAATGGCTCTTTTTCACCGCACGCACTGGCAAGGTCAGGTCAATT 540
DB 546 GCACCTGGCATTTAATGGCTCTTTTTCACCGCACGCACTGGCAAGGTCAGGTCAATT 605
QY 541 GATGCAAAATATGGTGAAGGAAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 600
DB 606 GATGCAAAATATGGTGAAGGAAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 665
QY 601 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTATTTGGATGGTGAGCACCTTTCTAT 660
DB 666 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTATTTGGATGGTGAGCACCTTTCTAT 725
QY 661 ACAGCTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC 720
DB 726 ACAGCTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC 785
QY 721 TACGAGTCTGTATCAAGAGACTTGGACTTAAAGTCTGATGAATTCCTCAATCAGATGAGC 780
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DB 786 TAGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 845
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTTGCAGATGTATTTGCAAAAGAGACGAAG 840
DB 846 ATGGATGATTGGCCAGAAATGAAGAAGATTTTGCAGATGTATTTGCAAAAGAGACGAAG 905
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCGTGTGTGACTCCGGTTCCTGACTTTT 900
DB 906 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCGTGTGTGACTCCGGTTCCTGACTTTT 965
QY 901 GAGGAGTGGTGTTCATCATGATCACAACAAGGAACCGGGCTCGTTATATCACAGTGAAGGAG 960
DB 966 GAGGAGTGGTGTTCATCATGATCACAACAAGGAACCGGGCTCGTTATATCACAGTGAAGGAG 1025
QY 961 CAGGACGTGAGCCCGCGCTCGACTCTGCTGTTAAACACCCAGCCATCCCTCTCTTC 1020
DB 1026 CAGGACGTGAGCCCGCGCTCGACTCTGCTGTTAAACACCCAGCCATCCCTCTCTTC 1085
QY 1021 AAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATTTCAGC 1080
DB 1086 AAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATTTCAGC 1145
QY 1081 CGCGAAGAGATTTATCAGCTTAATCAGATAAAATCAITTTGAAGTAATTAAGGTAAAGCT 1140
DB 1146 CGCGAAGAGATTTATCAGCTTAATCAGATAAAATCAITTTGAAGTAATTAAGGTAAAGCT 1205
QY 1141 AGTCTC 1146
DB 1206 AGTCTC 1211

RESULT 4
US-09-967-305-10
; Sequence 10, Application US/09967305
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1211)
US-09-967-305-10

Query Match      100.0%; Score 1146; DB 44; Length 2005;
Best Local Similarity 100.0%; Pred. No. 4.7e-290;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCGGCGCCGGTCTCTGT 60
DB 66 ATGGCACTGAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCGGCGCCGGTCTCTGT 125
QY 61 GCTATGCTCTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGACCGCGCGCTCCCGC 120
DB 126 GCTATGCTCTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGACCGCGCGCTCCCGC 185
QY 121 TAGACGTGAGCGCTTGGCGCGGCGCAAGCGCTCCGTAGTGTGACCTGAGCAGCGCG 180
DB 186 TAGACGTGAGCGCTTGGCGCGGCGCAAGCGCTCCGTAGTGTGACCTGAGCAGCGCG 245
QY 181 CGGGAGCGCGCTGCTCGCGCGCTGTGCAAGCGGTGCGATGCTGTGAGAGCCCTTC 240
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246 CGGGAGCGCGTCTGCGCGTCTGTGCAAGCGTGGATGCTGCTGGAGCCCTTC 305  
 Db  
 241 CGCCCGGTGTATGGAAGAACTCCAGCTGGGCCAGAGATTTGCGAGCGGAAAATCCA 300  
 Qy  
 306 CGCCCGGTGTATGGAAGAACTCCAGCTGGGCCAGAGATTTGCGAGCGGAAAATCCA 365  
 Db  
 301 AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAGCTTCTCGCGTTAGCT 360  
 Qy  
 366 AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAGCTTCTCGCGTTAGCT 425  
 Db  
 361 GGCACAGATATCAACTATTTGGCTTTGCTCAGGTGTTCTCTCAAAAATGGCAGAAGTGGT 420  
 Qy  
 426 GGCACAGATATCAACTATTTGGCTTTGCTCAGGTGTTCTCTCAAAAATGGCAGAAGTGGT 485  
 Db  
 421 GAGAACTCGATATGCGCGTGAATCTCTCGCTGATCTTGGTGGTGGCTTATGTTGT 480  
 Qy  
 486 GAGAACTCGATATGCGCGTGAATCTCTCGCTGATCTTGGTGGTGGCTTATGTTGT 545  
 Db  
 481 GCACCTGGATATTAATGGCTCTTTTGGCCAGCAGCAGCTGCGAAGGCTCAGGTCAAT 540  
 Qy  
 546 GCACCTGGATATTAATGGCTCTTTTGGCCAGCAGCAGCTGCGAAGGCTCAGGTCAAT 605  
 Db  
 541 GATGCAAAATATGTTGGAAGAACTGATATTTAAAGTTCTTTCTGTGAAAATCTCAGAAA 600  
 Qy  
 606 GATGCAAAATATGTTGGAAGAACTGATATTTAAAGTTCTTTCTGTGAAAATCTCAGAAA 665  
 Db  
 601 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTATTTGATGTTGGTGGTGGCTTCTAT 660  
 Qy  
 666 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTATTTGATGTTGGTGGTGGCTTCTAT 725  
 Db  
 661 ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720  
 Qy  
 726 ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 785  
 Db  
 721 TACGAGCTGCTGATCAAAAGGACTTTGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780  
 Qy  
 786 TACGAGCTGCTGATCAAAAGGACTTTGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 845  
 Db  
 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCAAAAGAGACGAAG 840  
 Qy  
 846 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCAAAAGAGACGAAG 905  
 Db  
 841 GCAGAGTGTGTCAAATCTTTGAGGACAGATGCTGTGACTCGGTTCTGACTTTT 900  
 Qy  
 906 GCAGAGTGTGTCAAATCTTTGAGGACAGATGCTGTGACTCGGTTCTGACTTTT 965  
 Db  
 901 GAGGAGTGTGTCATCATGATCAACAAGAGCGGCTCTGTTATCACCAGTGAAGGAG 960  
 Qy  
 966 GAGGAGTGTGTCATCATGATCAACAAGAGCGGCTCTGTTATCACCAGTGAAGGAG 1025  
 Db  
 961 CAGGAGCTGAGCCCGCCCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020  
 Qy  
 1026 CAGGAGCTGAGCCCGCCCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085  
 Db  
 1021 AAAAGGATCTTTTATAGAGAAACACACTGAGAGATATCTTGAAGAAATTTGATTCAGC 1080  
 Qy  
 1086 AAAAGGATCTTTTATAGAGAAACACACTGAGAGATATCTTGAAGAAATTTGATTCAGC 1145  
 Db  
 1081 CGGGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATCAAAAGTATTAAGTAAAGCT 1140  
 Qy  
 1146 CGGGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATCAAAAGTATTAAGTAAAGCT 1205  
 Db  
 1141 AGTCTC 1146  
 Qy  
 1206 AGTCTC 1211  
 Db

RESULT 5

US-10-210-120-104  
 ; Sequence 104, Application US/10210120  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chinnaiyan, Arul M.  
 ; APPLICANT: Rubin, Mark A.

APPLICANT: Sreekumar, Arun  
 ; TITLE OF INVENTION: Expression Profile of Prostate Cancer  
 ; FILE REFERENCE: UM-07221  
 ; CURRENT APPLICATION NUMBER: US/10/210,120  
 ; CURRENT FILING DATE: 2002-08-01  
 ; PRIOR APPLICATION NUMBER: US 60/309,581  
 ; PRIOR FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: US 60/334,468  
 ; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 123  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 104  
 ; LENGTH: 2005  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-210-120-104

no data > 2000

Query Match 100.0%; Score 1146; DB 50; Length 2005;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-290;  
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCACTGCGAGGGCATCTCGTCTGGAGCTGTCGGGCTGGCCCGGCGCCGCTTCTGT 60  
 Db 66 ATGGCACTGCGAGGGCATCTCGTCTGGAGCTGTCGGGCTGGCCCGGCGCCGCTTCTGT 125  
 Qy 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 126 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185  
 Qy 121 TACGAGCTGAGCGCTTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 Db 186 TACGAGCTGAGCGCTTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245  
 Qy 181 CGGGAGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 246 CGGGAGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305  
 Qy 241 CGCGCGGTGTCTATGAGAAATCCAGCTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 Db 306 CGCGCGGTGTCTATGAGAAATCCAGCTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365  
 Qy 301 AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAGCTTCTGCGGTTAGCT 360  
 Db 366 AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAGCTTCTGCGGTTAGCT 425  
 Qy 361 GGCACAGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATGGCAGAAGTGGT 420  
 Db 426 GGCACAGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATGGCAGAAGTGGT 485  
 Qy 421 GAGAACTCGATATGCGCGTGAATCTCTCGCTGACTTTGCTGGTGGTGGCTTATGTTGT 480  
 Db 486 GAGAACTCGATATGCGCGTGAATCTCTCGCTGACTTTGCTGGTGGTGGCTTATGTTGT 545  
 Qy 481 GCACCTGGATATTAATGGCTCTTTTGGCCAGCAGCAGCTGCGAAGGCTCAGGTCAAT 540  
 Db 546 GCACCTGGATATTAATGGCTCTTTTGGCCAGCAGCAGCTGCGAAGGCTCAGGTCAAT 605  
 Qy 541 GATGCAAAATATGTTGGAAGAACTGATATTTAAAGTTCTTTCTGTGAAAATCTCAGAAA 600  
 Db 606 GATGCAAAATATGTTGGAAGAACTGATATTTAAAGTTCTTTCTGTGAAAATCTCAGAAA 665  
 Qy 601 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTATTTGATGTTGGTGGTGGCTTCTAT 660  
 Db 666 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTATTTGATGTTGGTGGTGGCTTCTAT 725  
 Qy 661 ACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720  
 Db 726 ACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 785  
 Qy 721 TACGAGCTGCTGATCAAAAGGACTTTGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780  
 Db 786 TACGAGCTGCTGATCAAAAGGACTTTGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 845

QY 781 ATGGATGATGGCCAGCAATGAGAGAGAGTTTTCAGATGTATTTGCAAGAGACGAAG 840  
 DB |||||  
 QY 846 ATGGATGATGGCCAGCAATGAGAGAGAGTTTTCAGATGTATTTGCAAGAGACGAAG 905  
 DB |||||  
 QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCCTGACTTTT 900  
 DB |||||  
 QY 906 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCCTGACTTTT 965  
 DB |||||  
 QY 901 GAGGAGTGGTGTCAATCATGATATCAACAAGAGAACGGGGTCTGTTTATACACAGTGAAGAG 960  
 DB |||||  
 QY 966 GAGGAGTGGTGTCAATCATGATATCAACAAGAGAACGGGGTCTGTTTATACACAGTGAAGAG 1025  
 DB |||||  
 QY 961 CAGGAGTGGGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCATCCCTCTTTC 1020  
 DB |||||  
 QY 1026 CAGGAGTGGGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCATCCCTCTTTC 1085  
 DB |||||  
 QY 1021 AAAAGGATCTTTTCATAGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1080  
 DB |||||  
 QY 1086 AAAAGGATCTTTTCATAGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1145  
 DB |||||  
 QY 1081 CGGAAAGAGATTTATCAGCTTAATCAGATAAAATCAATGAAAGTAAAGGTAAAGCT 1140  
 DB |||||  
 QY 1146 CGGAAAGAGATTTATCAGCTTAATCAGATAAAATCAATGAAAGTAAAGGTAAAGCT 1205  
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 QY 1141 AGTCTC 1146  
 DB |||||  
 QY 1206 AGTCTC 1211

RESULT 6  
 PCT-US02-23913-17  
 ; Sequence 17, Application PC/TUS0223913  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc. et al.  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
 ; FILE REFERENCE: MRI-044PC  
 ; CURRENT APPLICATION NUMBER: PCT/US02/23913  
 ; CURRENT FILING DATE: 2002-07-25  
 ; PRIOR FILING DATE: 2001-07-25  
 ; PRIOR APPLICATION NUMBER: 60/307,982  
 ; PRIOR FILING DATE: 2001-07-25  
 ; PRIOR APPLICATION NUMBER: 60/314,356  
 ; PRIOR FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/325,020  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: 60/341,746  
 ; PRIOR FILING DATE: 2001-12-12  
 ; PRIOR APPLICATION NUMBER: 60/362,158  
 ; PRIOR FILING DATE: 2002-03-05  
 ; NUMBER OF SEQ ID NOS: 455  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17  
 ; LENGTH: 2069  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; PCT-US02-23913-17

Query Match 100.0%; Score 1146; DB 1; Length 2069;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-290;  
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGACGGGCATCTCGTGTGGAGTGTCTGGCTGGCCCGGCGCCGCTTCTGT 60  
 DB |||||  
 QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGGTGTGTACGCTGGACCGCGCGGCTCCCGC 120  
 DB |||||  
 QY 150 GCTATGGTCTGGCTGACTTCGGGGCGCGGTGTGTGTACGCTGGACCGCGCGGCTCCCGC 209  
 DB |||||  
 QY 121 TACGACGTGAGCGCTTTGGGCGCGGCAAGGCTCGCTAGTGTGGACCTGAAAGCAGCGG 180  
 DB |||||  
 QY 210 TACGACGTGAGCGCTTTGGGCGCGGCAAGGCTCGCTAGTGTGGACCTGAAAGCAGCGG 269

QY 181 CGGGAGCGCGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGTCTGCTGAGCCCTTC 240  
 DB |||||  
 QY 270 CGGGAGCGCGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGTCTGCTGAGCCCTTC 329  
 DB |||||  
 QY 241 CGCCCGGTGTCTCATGAGAGAACTCCAGGTGGGCCAGAGATTTCTGAGCGGGAATCCA 300  
 DB |||||  
 QY 330 CGCCCGGTGTCTCATGAGAGAACTCCAGGTGGGCCAGAGATTTCTGAGCGGGAATCCA 389  
 DB |||||  
 QY 301 AGGCTTATTTATGCGCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCTGCCGTTAGCT 360  
 DB |||||  
 QY 390 AGGCTTATTTATGCGCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCTGCCGTTAGCT 449  
 DB |||||  
 QY 361 GCGCAGGATATCAATTTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAGAGAGTGT 420  
 DB |||||  
 QY 450 GCGCAGGATATCAATTTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAGAGAGTGT 509  
 DB |||||  
 QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTTGTGGTGGTGGCTTATGTGT 480  
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 QY 510 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTTGTGGTGGTGGCTTATGTGT 569  
 DB |||||  
 QY 481 GCACCTGGGCAATTAATGAGCTCTTTTGAACGCAACGCACTGGCAAGGTCAGTCAAT 540  
 DB |||||  
 QY 570 GCACCTGGGCAATTAATGAGCTCTTTTGAACGCAACGCACTGGCAAGGTCAGTCAAT 629  
 DB |||||  
 QY 541 GATGCANAATATGCTGGAGGAAACAGATATTTTAAAGTCTTTTCTGTGGAAACTCAGAAA 600  
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 DB |||||  
 QY 690 TCGAGTCTGTGGAGGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT 749  
 DB |||||  
 QY 661 AGCACTTACAGACAGACAGATGGGAAATTCATGCTGTGGTGGAGCAATAGAACCCAGTTC 720  
 DB |||||  
 QY 750 AGCACTTACAGACAGACAGATGGGAAATTCATGCTGTGGTGGAGCAATAGAACCCAGTTC 809  
 DB |||||  
 QY 721 TAGGAGCTCTGATCAAAAGCACTTGACCTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780  
 DB |||||  
 QY 810 TAGGAGCTCTGATCAAAAGCACTTGACCTAAAGTCTGATGAACTTCCCAATCAGATGAGC 869  
 DB |||||  
 QY 781 ATGGATGATGGCCAGAAATGAAGAGAAAGTTTGCAGATGTATTTGCAAGAGACGAAG 840  
 DB |||||  
 QY 870 ATGGATGATGGCCAGAAATGAAGAGAAAGTTTGCAGATGTATTTGCAAGAGACGAAG 929  
 DB |||||  
 QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGACTTTT 900  
 DB |||||  
 QY 930 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGACTTTT 989  
 DB |||||  
 QY 901 GAGGAGTGTGTTCATCATGATCAACAGAGGACGGGGCTCGTTTATCACCAGTGAAGAG 960  
 DB |||||  
 QY 990 GAGGAGTGTGTTCATCATGATCAACAGAGGACGGGGCTCGTTTATCACCAGTGAAGAG 1049  
 DB |||||  
 QY 961 CAGGAGCTGAGCCCCCGCCCTGCACCTCTGCTTTAAACACCCCGCATCCCTCTTTC 1020  
 DB |||||  
 QY 1050 CAGGAGCTGAGCCCCCGCCCTGCACCTCTGCTTTAAACACCCCGCATCCCTCTTTC 1109  
 DB |||||  
 QY 1021 AAAAGGATCTTTTCATAGAGAAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1080  
 DB |||||  
 QY 1110 AAAAGGATCTTTTCATAGAGAAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGC 1169  
 DB |||||  
 QY 1081 CGGCAAGAGATTTATCAGCTTAATCAGATAAAATCAATGAAAGTAAAGGTAAAGCT 1140  
 DB |||||  
 QY 1170 CGGCAAGAGATTTATCAGCTTAATCAGATAAAATCAATGAAAGTAAAGGTAAAGCT 1229  
 DB |||||  
 QY 1141 AGTCTC 1146  
 DB |||||  
 QY 1230 AGTCTC 1235

RESULT 7  
 US-09-967-305-4  
 ; Sequence 4, Application US/09967305

GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE  
; FILE REFERENCE: 07334-312001  
; CURRENT APPLICATION NUMBER: US/09/967.305  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/236,238  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (90)...(1235)  
US-09-967-305-4

Query Match 100.0%; Score 1146; DB 44; Length 2069;  
Best Local Similarity 100.0%; Pred. No. 4.9e-290;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCACTGACGGGCACTCTGGTCTGGAGCTGTCCGGCTTGGCCCGGGCCGTTCTGT 60  
Db 90 ATGCACTGACGGGCACTCTGGTCTGGAGCTGTCCGGCTTGGCCCGGGCCGTTCTGT 149  
Qy 61 GCTATGCTCTGGCTGACTTCCGGGCGCTGTGTGCTAGCGTGGACCGGCGCTCCCGC 120  
Db 150 GCTATGCTCTGGCTGACTTCCGGGCGCTGTGTGCTAGCGTGGACCGGCGCTCCCGC 209  
Qy 121 TACGACGTGAGCGCTTTGGGCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 180  
Db 210 TACGACGTGAGCGCTTTGGGCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 269  
Qy 181 CGGGAGCGCGCTGCTGGCGCTCTGTGACAGCGGTGCGATGCTGTGGAGCCCTTC 240  
Db 270 CGGGAGCGCGCTGCTGGCGCTCTGTGACAGCGGTGCGATGCTGTGGAGCCCTTC 329  
Qy 241 CGCGCGGTGTGATGGAGAACTCCAGCTGGGCGCCAGAGATTCGACGGGGAAATCCA 300  
Db 330 CGCGCGGTGTGATGGAGAACTCCAGCTGGGCGCCAGAGATTCGACGGGGAAATCCA 389  
Qy 301 AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTAGCT 360  
Db 390 AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTAGCT 449  
Qy 361 GGCCACGATCAACTATTTGGCTTCTCAGGTGTTCTCAAAATTTGGCAGAGTGGT 420  
Db 450 GGCCACGATCAACTATTTGGCTTCTCAGGTGTTCTCAAAATTTGGCAGAGTGGT 509  
Qy 421 GAGAACCGTATGCGCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 510 GAGAACCGTATGCGCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569  
Qy 481 GCACCTGGCATTAATAAGTCTTTTTCACGACAGCTGCGCAAGGTTCAGGTCAAT 540  
Db 570 GCACCTGGCATTAATAAGTCTTTTTCACGACAGCTGCGCAAGGTTCAGGTCAAT 629  
Qy 541 GATGCAAAATATGTTGGAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 600  
Db 630 GATGCAAAATATGTTGGAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 689  
Qy 601 TCGAGTCTGGGAGACCTTCGAGGACAGAACTATGTTGGATGGTGGAGCACCTTTCTAT 660  
Db 690 TCGAGTCTGGGAGACCTTCGAGGACAGAACTATGTTGGATGGTGGAGCACCTTTCTAT 749  
Qy 661 ACAGCTTACAGGACAGCAGATGGGGAATTCATGCTGTGAGCAATAGAACCCAGTTC 720  
Db 750 ACAGCTTACAGGACAGCAGATGGGGAATTCATGCTGTGAGCAATAGAACCCAGTTC 809

Qy 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAAGTCTCCCAATCAGATGAGC 780  
Db 810 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAAGTCTCCCAATCAGATGAGC 869  
Qy 781 ATGATGATTTGGCCAGAAATGAAGAGAACTTTTGCAGATGATTTTGCAGAGAACGAAAG 840  
Db 870 ATGATGATTTGGCCAGAAATGAAGAGAACTTTTGCAGATGATTTTGCAGAGAACGAAAG 929  
Qy 841 GCAGAGTGGTGTCAAAATCTTTTGAAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 930 GCAGAGTGGTGTCAAAATCTTTTGAAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 989  
Qy 901 GAGGAGTGGTGTCAAAATCTTTTGAAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 990 GAGGAGTGGTGTCAAAATCTTTTGAAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049  
Qy 961 CAGGAGTGGAGCCCGCCCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 1050 CAGGAGTGGAGCCCGCCCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109  
Qy 1021 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1080  
Db 1110 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTCAGC 1169  
Qy 1081 CGGAGAGATTTATCAGCTTAACTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
Db 1170 CGGAGAGATTTATCAGCTTAACTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1229  
Qy 1141 AGTCTC 1146  
Db 1230 AGTCTC 1235

RESULT 8

US-10-205-823-17  
; Sequence 17, Application US/10205823  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gorbacheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Monsey, Angela M.  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Dustin  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-823-17

Query Match 100.0%; Score 1146; DB 50; Length 2069;

no / data > 2000



|  |      |  |      |  |  |  |  |  |  |
|--|------|--|------|--|--|--|--|--|--|
| Best Local Similarity 100.0%; Pred. No. 4.8e-290;<br>Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |      |  |      |  |  |  |  |  |  |
| Qy   | 1    | ATGGCACTGAGGGCATCTCGTGTGGAGACTGTGCGGCTGCGCCCGGCGCCGTTCTGT    | 60   |  |  |  |  |  |  |
| Db   | 90   | ATGGCACTGAGGGCATCTCGTGTGGAGACTGTGCGGCTGCGCCCGGCGCCGTTCTGT    | 149  |  |  |  |  |  |  |
| Qy   | 61   | GCTATGCTGCTGGCTGACTTTCGGGGCGGTGTGGTACGCGTGGACCGGCGCGCTCCCG   | 120  |  |  |  |  |  |  |
| Db   | 150  | GCTATGCTGCTGGCTGACTTTCGGGGCGGTGTGGTACGCGTGGACCGGCGCGCTCCCG   | 209  |  |  |  |  |  |  |
| Qy   | 121  | TACGACGTGAGCGCTTGGCGCGGGCAAGCGTCTGCTAGTGTGGAACCTGAAGACGCG    | 180  |  |  |  |  |  |  |
| Db   | 210  | TACGACGTGAGCGCTTGGCGCGGGCAAGCGTCTGCTAGTGTGGAACCTGAAGACGCG    | 269  |  |  |  |  |  |  |
| Qy   | 181  | CGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGTGTGCTGTGCTGTGAGCGCTTC       | 240  |  |  |  |  |  |  |
| Db   | 270  | CGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGTGTGCTGTGCTGTGAGCGCTTC       | 329  |  |  |  |  |  |  |
| Qy   | 241  | CGCGCGGTGTGATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGGAATCCA     | 300  |  |  |  |  |  |  |
| Db   | 330  | CGCGCGGTGTGATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGGAATCCA     | 389  |  |  |  |  |  |  |
| Qy   | 301  | AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTTAGCT    | 360  |  |  |  |  |  |  |
| Db   | 390  | AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTTAGCT    | 449  |  |  |  |  |  |  |
| Qy   | 361  | GGCCACGATCAACTATTTGGCTTTCTCAGGTGTTCTCTCAAAAATGGCAGAGTGT      | 420  |  |  |  |  |  |  |
| Db   | 450  | GGCCACGATCAACTATTTGGCTTTCTCAGGTGTTCTCTCAAAAATGGCAGAGTGT      | 509  |  |  |  |  |  |  |
| Qy   | 421  | GAGNATCCGTATGCCCGCTGAATCTCTCGCTGACTTTGCTGGTGGCTTATGTGT       | 480  |  |  |  |  |  |  |
| Db   | 510  | GAGNATCCGTATGCCCGCTGAATCTCTCGCTGACTTTGCTGGTGGCTTATGTGT       | 569  |  |  |  |  |  |  |
| Qy   | 481  | GCACCTGGGCATTATAATGGCTCTTTTTCGCGCACAGCACTGCGAAGGTCAAGTCATT   | 540  |  |  |  |  |  |  |
| Db   | 570  | GCACCTGGGCATTATAATGGCTCTTTTTCGCGCACAGCACTGCGAAGGTCAAGTCATT   | 629  |  |  |  |  |  |  |
| Qy   | 541  | GATGCAAAATATGTTGGAAGCAACAGCATATTTAAGTTCTTTTCTGTGGAATACTAGAAA | 600  |  |  |  |  |  |  |
| Db   | 630  | GATGCAAAATATGTTGGAAGCAACAGCATATTTAAGTTCTTTTCTGTGGAATACTAGAAA | 689  |  |  |  |  |  |  |
| Qy   | 601  | TCGAGTCTGTGGAGACCACTCGAGGACAGAAATGTTGATGGTGGAGCACCTTTCTAT    | 660  |  |  |  |  |  |  |
| Db   | 690  | TCGAGTCTGTGGAGACCACTCGAGGACAGAAATGTTGATGGTGGAGCACCTTTCTAT    | 749  |  |  |  |  |  |  |
| Qy   | 661  | ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC    | 720  |  |  |  |  |  |  |
| Db   | 750  | ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC    | 809  |  |  |  |  |  |  |
| Qy   | 721  | TACGAGTCTGTATCAAAAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC  | 780  |  |  |  |  |  |  |
| Db   | 810  | TACGAGTCTGTATCAAAAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC  | 869  |  |  |  |  |  |  |
| Qy   | 781  | ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGAAG     | 840  |  |  |  |  |  |  |
| Db   | 870  | ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGAAG     | 929  |  |  |  |  |  |  |
| Qy   | 841  | GCAGATGTTGTAATCTTTTTCGCGCACAGATGCTGTGACTCCGGTCTCTGACTTTT     | 900  |  |  |  |  |  |  |
| Db   | 930  | GCAGATGTTGTAATCTTTTTCGCGCACAGATGCTGTGACTCCGGTCTCTGACTTTT     | 989  |  |  |  |  |  |  |
| Qy   | 901  | GAGGAGTTGTTATCATATGATCAACAAGGAAGCGGGCTCGTTTATCAGAGTGGAG      | 960  |  |  |  |  |  |  |
| Db   | 990  | GAGGAGTTGTTATCATATGATCAACAAGGAAGCGGGCTCGTTTATCAGAGTGGAG      | 1049 |  |  |  |  |  |  |
| Qy   | 961  | CAGGAGTGTAGCCCCCTGACCTCTGCTGTATAAACCAGCCAGCCATCCCTTCTTC      | 1020 |  |  |  |  |  |  |
| Db   | 1050 | CAGGAGTGTAGCCCCCTGACCTCTGCTGTATAAACCAGCCAGCCATCCCTTCTTC      | 1109 |  |  |  |  |  |  |
| Qy   | 1021 | AAAAGGATCTCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGATTCAGC  | 1080 |  |  |  |  |  |  |

RESULT 9

US-60-601-413-3

; Sequence 3, Application US/60601413

; GENERAL INFORMATION:

; APPLICANT: Monahan, John

; APPLICANT: Kamatkar, Shubhangi

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Gorbacheva, Bella

; APPLICANT: Glatt, Karen

; APPLICANT: Ford, Donna

; APPLICANT: Endege, Wilson

; APPLICANT: Anderson, Dustin

; TITLE OF INVENTION: GENES, COMPOSITIONS, KITS, AND METHODS

; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

; TITLE OF INVENTION: PROSTATE CANCER

; FILE REFERENCE: MPI04-017PIM

; CURRENT APPLICATION NUMBER: US/60/601,413

; CURRENT FILING DATE: 2004-08-13

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 3184

; TYPE: DNA

; ORGANISM: human

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (90) .... (1238)

US-60-601-413-3

Query Match

Best Local Similarity 100.0%; Score 1146; DB 69; Length 3184;

Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | ATGGCACTGAGGGCATCTCGTGTGGAGACTGTGCGGCTGCGCCCGGCGCCGTTCTGT  | 60  |
| Db | 90  | ATGGCACTGAGGGCATCTCGTGTGGAGACTGTGCGGCTGCGCCCGGCGCCGTTCTGT  | 149 |
| Qy | 61  | GCTATGCTGCTGGCTGACTTTCGGGGCGGTGTGGTACGCGTGGACCGGCGCGCTCCCG | 120 |
| Db | 150 | GCTATGCTGCTGGCTGACTTTCGGGGCGGTGTGGTACGCGTGGACCGGCGCGCTCCCG | 209 |
| Qy | 121 | TACGACGTGAGCGCTTGGCGCGGGCAAGCGTCTGCTAGTGTGGAACCTGAAGACGCG  | 180 |
| Db | 210 | TACGACGTGAGCGCTTGGCGCGGGCAAGCGTCTGCTAGTGTGGAACCTGAAGACGCG  | 269 |
| Qy | 181 | CGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGTGTGCTGTGCTGTGAGCGCTTC     | 240 |
| Db | 270 | CGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGTGTGCTGTGCTGTGAGCGCTTC     | 329 |
| Qy | 241 | CGCGCGGTGTGATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGGAATCCA   | 300 |
| Db | 330 | CGCGCGGTGTGATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGGAATCCA   | 389 |
| Qy | 301 | AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTTAGCT  | 360 |
| Db | 390 | AGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTTAGCT  | 449 |
| Qy | 361 | GGCCACGATCAACTATTTGGCTTTCTCAGGTGTTCTCTCAAAAATGGCAGAGTGT    | 420 |
| Db | 450 | GGCCACGATCAACTATTTGGCTTTCTCAGGTGTTCTCTCAAAAATGGCAGAGTGT    | 509 |
| Qy | 421 | GAGNATCCGTATGCCCGCTGAATCTCTCGCTGACTTTGCTGGTGGCTTATGTGT     | 480 |

no. 1146 > 2000





Db 1110 AAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1169  
Qy 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAATAATCATTTGAAGTAATTAAGTAAAGCT 1140  
Db 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATAAATAATCATTTGAAGTAATTAAGTAAAGCT 1229  
Qy 1141 AGTCTC 1146  
Db 1230 AGTCTC 1235

RESULT 11  
US-10-170-235-26493  
; Sequence 26493, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
; FILE REFERENCE: CL001380  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 26493  
; LENGTH: 2045  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-26493

Query Match 99.9%; Score 1144.4; DB 49; Length 2045;  
Best Local Similarity 99.9%; Pred. No. 1.3e-289;  
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCAGTCTGAGGAGATCTCGTCTGAGAGCTGTGCGGCTGCGCCCGGCGCCCGTCTGT 60  
Db 90 ATGGCAGTCTGAGGAGATCTCGTCTGAGAGCTGTGCGGCTGCGCCCGGCGCCCGTCTGT 149

Qy 61 GCTATGCTGCTGCTGACTTTCGGGGCGCGTGTGCTAGCGGTGACCGCGCCGCTCCCG 120  
Db 150 GCTATGCTGCTGCTGACTTTCGGGGCGCGTGTGCTAGCGGTGACCGCGCCGCTCCCG 209

Qy 121 TAGCAGCTGAGCGCTTTGGCGCGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCAGCGG 180  
Db 210 TAGCAGCTGAGCGCTTTGGCGCGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCAGCGG 269

Qy 181 CGGGAGCGCGCTGCTGCGGCGCTGTGCAAGGGTTCGATGCTGCTGAGAGCGCTTC 240  
Db 270 CGGGAGCGCGCTGCTGCGGCGCTGTGCAAGGGTTCGATGCTGCTGAGAGCGCTTC 329

Qy 241 CGCGCGGCTGCTATGGAGAACTCCAGCTCGGCGCCAGAGATTCTGCAGCGGGAATAATCCA 300  
Db 330 CGCGCGGCTGCTATGGAGAACTCCAGCTCGGCGCCAGAGATTCTGCAGCGGGAATAATCCA 389

Qy 301 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTTCAGGAAGCTTCTCGCGGTAGCT 360  
Db 390 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTTCAGGAAGCTTCTCGCGGTAGCT 449

Qy 361 GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATGGCAGAGTGGT 420  
Db 450 GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATGGCAGAGTGGT 509

Qy 421 GAGAACTCGATGCGCGCTGATCTCCTCGCTGACCTTCTGCTGGTGGCTTTATGCTGT 480  
Db 510 GAGAACTCGATGCGCGCTGATCTCCTCGCTGACCTTCTGCTGGTGGCTTTATGCTGT 569

Qy 481 GCACCTGGGCAATTAATAGGCTCTTTTTCACCGCACACGACACTGGCAAGGCTCAGGTCAAT 540  
Db 570 GCACCTGGGCAATTAATAGGCTCTTTTTCACCGCACACGACACTGGCAAGGCTCAGGTCAAT 629

Qy 541 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTCTGTGGAAAACTCAGAAA 600  
Db 630 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTCTGTGGAAAACTCAGAAA 689

Qy 601 TCGAGTCTGTGGGAAGCACCTCGAGGAGACAGAACTGTTGGATGCTGGAGCACCTTTCTAT 660

value > 1000

Db 690 TCGAGTCTGTGGAAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 749  
Qy 661 AGCACTTACAGACAGCAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720  
Db 750 AGCACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 809  
Qy 721 TAGGAGTCTGATCAAAAGGACTTTGAGCTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780  
Db 810 TAGGAGTCTGATCAAAAGGACTTTGAGCTAAAGTCTGATGAACCTCCCAATCAGATGAGC 869  
Qy 781 ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTGCAAGAAGACGAAG 840  
Db 870 ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTGCAAGAAGACGAAG 929  
Qy 841 GGAGAGTGTGTCAAAATCTTTTACCGCACAGATGCTGTGACTCCGTTCTGACTTTT 900  
Db 930 GGAGAGTGTGTCAAAATCTTTTACCGCACAGATGCTGTGACTCCGTTCTGACTTTT 989  
Qy 901 GAGGAGTGTGTCAATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 960  
Db 990 GAGGAGTGTGTCAATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 1049  
Qy 961 GAGGAGTGTGTCAATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 1020  
Db 1050 GAGGAGTGTGTCAATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 1109  
Qy 1021 AAAAGGATCTTTTATAGGAGAAACACTGAGGAGATCTTGAAGAAATTTGATTCAGC 1080  
Db 1110 AAAAGGATCTTTTATAGGAGAAACACTGAGGAGATCTTGAAGAAATTTGATTCAGC 1169  
Qy 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAATAATCATTTGAAAGTAATTAAGTAAAGCT 1140  
Db 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATAAATAATCATTTGAAAGTAATTAAGTAAAGCT 1229

Qy 1141 AGTCTC 1146  
Db 1230 AGTCTC 1235

RESULT 12  
PCT-US02-23913-25  
; Sequence 25, Application PC/TUS0223913  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
; FILE REFERENCE: MRI-044PC  
; CURRENT APPLICATION NUMBER: PCT/US02/23913  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-23913-25

Query Match 99.9%; Score 1144.4; DB 1; Length 2069;  
Best Local Similarity 99.9%; Pred. No. 1.3e-289;  
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

value > 1000

QY 1 ATGGCACTGAGGCACTCTCGGTCTGGAGCTGTCCGGCTTGGCCCGGCGCGTCTGT 60  
Db 90 ATGGCACTGAGGCACTCTCGGTCTGGAGCTGTCCGGCTTGGCCCGGCGCGTCTGT 149  
QY 61 GCTATGCTCTGGCTGACTTTCGGGGCGGTGTGGTACGGCTGACCGGCGCGCTCCCG 120  
Db 150 GCTATGCTCTGGCTGACTTTCGGGGCGGTGTGGTACGGCTGACCGGCGCGCTCCCG 209  
QY 121 TAGCAGCTGAGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 180  
Db 210 TAGCAGCTGAGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGT 269  
QY 181 CGGGGAGCGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 240  
Db 270 CGGGGAGCGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 329  
QY 241 CGCGCGGCTGTCTATGAGAACTCCAGCTGGGCGCGAGAGATCTGACGGGGAATCC 300  
Db 330 CGCGCGGCTGTCTATGAGAACTCCAGCTGGGCGCGAGAGATCTGACGGGGAATCC 389  
QY 301 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCGAGTTCAGAAAGCTTTCGCCGTTAG 360  
Db 390 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCGAGTTCAGAAAGCTTTCGCCGTTAG 449  
QY 361 GGCACGATATCAATTTGGCTTGTCTAGGTGTCTCTCAAAATTTGCGCAAGTGT 420  
Db 450 GGCACGATATCAATTTGGCTTGTCTAGGTGTCTCTCAAAATTTGCGCAAGTGT 509  
QY 421 GAGAATCCGATGCGCGCTGAATCTCTGGCTGACTTTCGCTGGTGGCTTATGTGT 480  
Db 510 GAGATCCGATGCGCGCTGAATCTCTGGCTGACTTTCGCTGGTGGCTTATGTGT 569  
QY 481 GCATGGGCAATTAATGGCTCTTTTTCGCGCACGACGCTGCGCAAGGCTCAGGTCA 540  
Db 570 GCATGGGCAATTAATGGCTCTTTTTCGCGCACGACGCTGCGCAAGGCTCAGGTCA 629  
QY 541 GATGCAATATGTTGAGAGAAACAGCATATTTAAGTCTTTTCTGTGGAAATCAGAAA 600  
Db 630 GATGCAATATGTTGAGAGAAACAGCATATTTAAGTCTTTTCTGTGGAAATCAGAAA 689  
QY 601 TCGAGTCTGTGGAGAGCACTTCGAGGACAGAAATGTTGGATGTTGGAGCACTTCTAT 660  
Db 690 TCGAGTCTGTGGAGAGCACTTCGAGGACAGAAATGTTGGATGTTGGAGCACTTCTAT 749  
QY 661 ACGACTTACAGGACAGCAGATGGGAAATCATGGCTGTTGGAGCAATAGAACCCAGTTC 720  
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QY 721 TAGCAGCTGCTATCAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAG 780  
Db 810 TAGCAGCTGCTATCAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAG 869  
QY 781 ATGGATGTTGGCGCAGAAATGAAGAGAGATTTGCGAGATGATTTGCAAGAGAGAGAG 840  
Db 870 ATGGATGTTGGCGCAGAAATGAAGAGAGATTTGCGAGATGATTTGCAAGAGAGAGAG 929  
QY 841 GCAGAGTGTGTCAAAATCTTTGACGCGCACAGATGCTGTGTGACTCCGGTTCGACTTTT 900  
Db 930 GCAGAGTGTGTCAAAATCTTTGACGCGCACAGATGCTGTGTGACTCCGGTTCGACTTTT 989  
QY 901 GAGGAGTGTGTTCATCATGATCAACAAGGAAACGGGGCTGTTTTATCACAGTGGAGAG 960  
Db 990 GAGGAGTGTGTTCATCATGATCAACAAGGAAACGGGGCTGTTTTATCACAGTGGAGAG 1049  
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QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAAGGTAAAGCT 1140

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Db 1230 AGTCTC 1235  
RESULT 13  
US-10-205-823-25  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gorbacheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Monsey, Angela M.  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Dustin  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; PRIOR FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-823-25  
Query Match 99.9%; Score 1144.4; DB 50; Length 2069;  
Best Local Similarity 99.9%; Pred. No. 1.3e-289;  
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGGCACTGAGGCACTCTCGGTCTGGAGCTGTCCGGCTTGGCCCGGCGCGTCTGT 60  
Db 90 ATGGCACTGAGGCACTCTCGGTCTGGAGCTGTCCGGCTTGGCCCGGCGCGTCTGT 149  
QY 61 GCTATGCTCTGGCTGACTTTCGGGGCGGTGTGGTACGGCTGACCGGCGCGCTCCCG 120  
Db 150 GCTATGCTCTGGCTGACTTTCGGGGCGGTGTGGTACGGCTGACCGGCGCGCTCCCG 209  
QY 121 TAGCAGCTGAGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 180  
Db 210 TAGCAGCTGAGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGT 269  
QY 181 CGGGGAGCGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 240  
Db 270 CGGGGAGCGCGCTTGGCGCGGCGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 329  
QY 241 CGCGCGGCTGTCTATGAGAACTCCAGCTGGGCGCGAGAGATCTGACGGGGAATCC 300  
Db 330 CGCGCGGCTGTCTATGAGAACTCCAGCTGGGCGCGAGAGATCTGACGGGGAATCC 389  
QY 301 AGGCTTATTTATGCGAGGCTGAGTGGATTTGGCGAGTTCAGAAAGCTTTCGCCGTTAG 360

1667 7000





Db 1145 AGTCTC 1150

Search completed: July 27, 2005, 10:25:21  
Job time : 5005 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:00:01 ; Search time 4256 Seconds  
(without alignments)  
10249.448 Million cell updates/sec

Title: US-09-967-305-3

Perfect score: 1146

Sequence: 1 atggcactgcaggcatctc.....ataaggtaaaagtagtctc 1146

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 1044  | 91.1        | 1544   | 3     | CR615811 full-leng |
| 2          | 1044  | 91.1        | 1967   | 3     | CR625004 full-leng |
| 3          | 1044  | 91.1        | 3111   | 3     | CR616479 full-leng |
| 4          | 762   | 66.5        | 977    | 1     | AL558928           |
| 5          | 664   | 57.9        | 890    | 5     | BQ62523 AGENCOURT  |
| 6          | 635   | 55.4        | 955    | 4     | BG741165           |
| 7          | 601   | 52.4        | 1081   | 1     | AL545355           |
| 8          | 589   | 51.4        | 649    | 5     | BQ638373           |
| 9          | 572   | 49.9        | 808    | 4     | B1256255           |
| 10         | 572   | 49.9        | 893    | 1     | AL558977           |
| 11         | 568   | 49.6        | 622    | 7     | CN305057           |
| 12         | 567   | 49.5        | 890    | 5     | BQ941482           |
| 13         | 562   | 49.0        | 613    | 7     | CN305056           |
| 14         | 561   | 49.0        | 812    | 4     | BG035606           |
| 15         | 552   | 48.2        | 583    | 5     | BP318564           |
| 16         | 552   | 48.2        | 1598   | 3     | CR618063           |
| 17         | 534   | 46.6        | 633    | 5     | BX099124           |
| 18         | 530   | 46.2        | 935    | 4     | BG286300           |
| 19         | 528   | 46.1        | 880    | 4     | BG289921           |
| 20         | 524   | 45.7        | 720    | 1     | AU117376           |
| 21         | 519   | 45.3        | 1076   | 1     | AL555978           |
| 22         | 507   | 44.2        | 713    | 1     | AV714764           |
| 23         | 501   | 43.7        | 583    | 5     | BP275107           |
| 24         | 498   | 43.5        | 729    | 4     | BI550368           |

|    |     |      |     |   |          |
|----|-----|------|-----|---|----------|
| 25 | 498 | 43.5 | 871 | 5 | EX449005 |
| 26 | 468 | 40.8 | 588 | 5 | BP239487 |
| 27 | 460 | 40.1 | 693 | 4 | BG779839 |
| 28 | 456 | 39.8 | 958 | 5 | BP390793 |
| 29 | 436 | 38.0 | 581 | 5 | BP276627 |
| 30 | 435 | 38.0 | 582 | 5 | BP221988 |
| 31 | 434 | 37.9 | 582 | 5 | BP199866 |
| 32 | 432 | 37.7 | 583 | 5 | BP260668 |
| 33 | 429 | 37.4 | 451 | 7 | CF142100 |
| 34 | 403 | 35.2 | 805 | 6 | CD643323 |
| 35 | 396 | 34.6 | 585 | 5 | BP261417 |
| 36 | 394 | 34.4 | 530 | 7 | CN305058 |
| 37 | 394 | 34.4 | 705 | 4 | BI597403 |
| 38 | 394 | 34.4 | 829 | 4 | BG708726 |
| 39 | 393 | 34.3 | 641 | 4 | BM829952 |
| 40 | 393 | 34.3 | 677 | 6 | CB268128 |
| 41 | 391 | 34.1 | 672 | 4 | BM714377 |
| 42 | 391 | 34.1 | 823 | 4 | BM723657 |
| 43 | 386 | 33.7 | 938 | 2 | BE622419 |
| 44 | 385 | 33.6 | 943 | 4 | BG289079 |
| 45 | 383 | 33.4 | 581 | 5 | BP311844 |

## ALIGNMENTS

|                       |  |   |           |              |                 |
|-----------------------|--|---|-----------|--------------|-----------------|
| RESULT 1              | CR615811   | 1544 bp   | mRNA      | linear       | HTC 21-JUL-2004 |
| LOCUS                 | full-length cDNA clone CSODI027YU12 of Placenta Cot 25-normalized  |   |           |              |                 |
| DEFINITION            | of Homo sapiens (human).   |   |           |              |                 |
| ACCESSION             | CR615811   |   |           |              |                 |
| VERSION               | CR615811.1   | GI:50496618   |           |              |                 |
| KEYWORDS              | HTC; CNSLT CDNA.   |   |           |              |                 |
| SOURCE                | Homo sapiens (human)   |   |           |              |                 |
| ORGANISM              | Homo sapiens   |   |           |              |                 |
| REFERENCE             | 1 (bases 1 to 1544)  |   |           |              |                 |
| AUTHORS               | Li, W.B., Gruber, C., Jessee, J. and Polayes, D.   |   |           |              |                 |
| TITLE                 | Full-length cDNA libraries and normalization   |   |           |              |                 |
| JOURNAL               | Unpublished  |   |           |              |                 |
| REMARK                | Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue  |   |           |              |                 |
| REFERENCE             | 2 (bases 1 to 1544)  |   |           |              |                 |
| AUTHORS               | Genoscope.   |   |           |              |                 |
| TITLE                 | Direct Submission  |   |           |              |                 |
| JOURNAL               | Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr   |   |           |              |                 |
| COMMENT               | - Web : www.genoscope.cns.fr)<br>1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. |   |           |              |                 |
| FEATURES              | Location/Qualifiers  |   |           |              |                 |
| source                | 1..1544  |   |           |              |                 |
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|                       | /mol_type="mRNA"   |   |           |              |                 |
|                       | /db_xref="taxon:9606"  |   |           |              |                 |
|                       | /clones="CSODI027YU12"   |   |           |              |                 |
|                       | /tissue_type="Placenta Cot 25-normalized"  |   |           |              |                 |
|                       | /plasmid="pCMVSPORT_6"   |   |           |              |                 |
| ORIGIN                |  |   |           |              |                 |
| Query Match           | 91.1%;   | Score 1044;   | DB 3;     | Length 1544; |                 |
| Best Local Similarity | 99.8%;   | Pred. No. 0;  |           |              |                 |
| Matches 1144;         | Conservative 0;  | Mismatches 2;   | Indels 0; | Gaps 0;      |                 |
| Qy                    | 1  | ATGGCACTGCAGGCATCTCGTCTGTCGAGCTGTCGGCTGCGCCGCCGGCCGTTCTGT | 60        |              |                 |
| Db                    | 10   | ATGGCACTGCAGGCATCTCGTCTGTCGAGCTGTCGGCTGCGCCGCCGGCCGTTCTGT | 69        |              |                 |

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Qy 61 GCTATGTCCTGGCTGACTTCGGGCGCGTGTGGTACGCGTGAGCCGCGCGCTCCGCG 120
Db 70 GCTATGTCCTGGCTGACTTCGGGCGCGTGTGGTACGCGTGAGCCGCGCGCTCCGCG 129

Qy 121 TACGACGTGAGCGCTTGGCGGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCG 180
Db 130 TACGACGTGAGCGCTTGGCGGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCG 189

Qy 181 CGGGAGCGCGTCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTCTGGAGCCCTTC 240
Db 190 CGGGAGCGCGTCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTCTGGAGCCCTTC 249

Qy 241 CGCCGCGTGTGTCAGAGAACTCCAGCTGGGCCAGAGATTCGCGCGGGAATAATCCA 300
Db 250 CGCCGCGTGTGTCAGAGAACTCCAGCTGGGCCAGAGATTCGCGCGGGAATAATCCA 309

Qy 301 AGGCTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCGGTTAGCT 360
Db 310 AGGCTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCGGTTAGCT 369

Qy 361 GGCACGATATCACTATTGGCTTTGTGACGTTCTCTCAAAATTTGGCAGAGTGT 420
Db 370 GGCACGATATCACTATTGGCTTTGTGACGTTCTCTCAAAATTTGGCAGAGTGT 429

Qy 421 GAGATCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGTGGTGGCTTATGTT 480
Db 430 GAGATCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGTGGTGGCTTATGTT 489

Qy 481 GCACCTGGGCATTATATGGCTCTTTTTCACCGCACACGCTGGAAGGTCAGTCAAT 540
Db 490 GCACCTGGGCATTATATGGCTCTTTTTCACCGCACACGCTGGAAGGTCAGTCAAT 549

Qy 541 GATCAAAATATGTTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAATCTCAGAAA 600
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Qy 601 TCGAGCTGTGGGAGACCTCGAGGACAGACATGTTGGATGTTGGAGCACCTTCTAT 660
Db 610 TCGAGCTGTGGGAGACCTCGAGGACAGACATGTTGGATGTTGGAGCACCTTCTAT 669

Qy 661 ACGACTTACGACGACGAGATGGGAAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 720
Db 670 ACGACTTACGACGACGAGATGGGAAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 729

Qy 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780
Db 730 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 789

Qy 781 ATGGATGATTCGCCAGAAATGAGGAAGTTTGCAGATGATTTTGCAGGAAGACGGAAG 840
Db 790 ATGGATGATTCGCCAGAAATGAGGAAGTTTGCAGATGATTTTGCAGGAAGACGGAAG 849

Qy 841 CGAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTTCCGGTCTGACTTTT 900
Db 850 CGAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTTCCGGTCTGACTTTT 909

Qy 901 GAGGAGTGTGTTTCATCATGATCACAACAAAGGAAACGGGGCTGTTTATCACCAGTGAGGAG 960
Db 910 GAGGAGTGTGTTTCATCATGATCACAACAAAGGAAACGGGGCTGTTTATCACCAGTGAGGAG 969

Qy 961 CAGGAGCTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTCTTTC 1020
Db 970 CAGGAGCTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTCTTTC 1029

Qy 1021 AAAAGGATCTCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1080
Db 1030 AAAAGGATCTCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1089

Qy 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAATTAAGGTAAAGCT 1140
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Qy 1141 AGTCTC 1146
Db 1150 AGTCTC 1155

RESULT 2
CR625004 1967 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DJ007Y107 of T cells (Jurkat cell line)
DEFINITION Cot 10-normalized of Homo sapiens (human).
ACCESSION CR625004
VERSION CR625004.1 GI:50505811
KEYWORDS HTC; CNSLT CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1967)
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1967)
REFERENCE 2
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ007Y107"
/tissue_type="T cells (Jurkat cell line) Cot
10-normalized"
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ORIGIN
Query Match 91.1%; Score 1044; DB 3; Length 1967;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGSCACTGCAGGCGATCTCGGTCTGTGAGCTGTCCGGCTTGGCCCGCGGCGCTTCTGT 60
Db 45 ATGSCACTGCAGGCGATCTCGGTCTGTGAGCTGTCCGGCTTGGCCCGCGGCGCTTCTGT 104

Qy 61 GCTATGTCCTGGCTGACTTCGGGCGCGTGTGGTACGCGTGAGCCGCGCGCTCCGCG 120
Db 105 GCTATGTCCTGGCTGACTTCGGGCGCGTGTGGTACGCGTGAGCCGCGCGCTCCGCG 164

Qy 121 TACGACGTGAGCGCTTGGCGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCG 180
Db 165 TACGACGTGAGCGCTTGGCGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCG 224

Qy 181 CGGGAGCGCGTCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTCTGGAGCCCTTC 240
Db 225 CGGGAGCGCGTCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTCTGGAGCCCTTC 284

Qy 241 CGCGCGGTGTCTAGGAGAACTCCAGCTGGGCCAGAGATTCGCGCGGGAATAATCCA 300
Db 285 CGCGCGGTGTCTAGGAGAACTCCAGCTGGGCCAGAGATTCGCGCGGGAATAATCCA 344

Qy 301 AGGCTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 360
Db 345 AGGCTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 404
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QY 361 GCCACGATATCAACTATTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAGAGTGGT 420  
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 QY 421 GAGAAATCGGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTT 480  
 Db 465 GAGAAATCGGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTT 524  
 QY 481 GCATGGGATTAATATGCTCTTTTTCACCGCACACGACCTGGCAAGGTCAGTCAATT 540  
 Db 525 GCATGGGATTAATATGCTCTTTTTCACCGCACACGACCTGGCAAGGTCAGTCAATT 584  
 QY 541 GATGCAATATGTTGGAAGAACAGATATTTAAGTCTTTTCTGTGGAATCTCAGAAA 600  
 Db 585 GATGCAATATGTTGGAAGAACAGATATTTAAGTCTTTTCTGTGGAATCTCAGAAA 644  
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 Db 645 TTGAGTCTGTGGGAAGACCTCGAGGACAGCAATGTTGGATGTTGGAGGACCTTTCTAT 704  
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 Db 765 TACGAGTCTGTATCAAGAGACTTGGACTAAGTCTGATGAATTTCCCAATCAGATGAGC 824  
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 QY 1081 CGCGAAGAGATTTATCAGCTTAATCTCAGATAAAATCATTTGAAGTAATAGSTAAAGCT 1140  
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RESULT 3  
 LOCUS CR616479 3111 bp mRNA linear HTC 21-JUL-2004  
 DEFINITION full-length cDNA clone CS0DK010Y111 of HeLa cells Cot 25-normalized of Homo sapiens (human).  
 ACCESSION CR616479  
 VERSION CR616479.1 GI:50497286  
 KEYWORDS HTC; CNSLT\_cDNA.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 3111)  
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished  
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue  
 2 (bases 1 to 3111)  
 Genoscope.  
 Direct Submission  
 JOURNAL  
 TITLE  
 AUTHORS  
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
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 /clone="CS0DK010Y111"  
 /tissue\_type="HeLa cells Cot 25-normalized"  
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 Db 77 ATGCGACTGACAGGCACTCTCGGTCTGTGGAGCTGTCCGCTTGGCCCGGCGCTTCTGT 136  
 QY 61 GCTATGCTCTGCTGACTTCCGGCGCGGTGTGTGACGCTGGACCGCCCGCTCCGCG 120  
 Db 137 GCTATGCTCTGCTGACTTCCGGCGCGGTGTGTGACGCTGGACCGCCCGCTCCGCG 196  
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 Db 197 TACGACGTGAGCCGCTTTGGCCCGGCAAGCGCTCGTGTAGTGTGACCTTGAAGCAGCG 256  
 QY 181 CGGAGGCGCGCGCTGTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 240  
 Db 257 CGGAGGCGCGCGCTGTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 316  
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 QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAGTGGT 420  
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 QY 421 GAGAAATCGGTATGCCCGCTGAATCTCTGCTGACTTTGCTGGTGGCTTATGTT 480  
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 Db 557 GCATGGGATTAATATGCTCTTTTTCACCGCACACGACCTGGCAAGGTCAGTCAATT 616  
 QY 541 GATGCAATATGTTGGAAGAACAGATATTTAAGTCTTTTCTGTGGAATCTCAGAAA 600  
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RESULT 4  
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 DEFINITION Homo sapiens cDNA clone CS0DJ007Y107 5-PRIME, mRNA sequence.  
 ACCESSION AL558928  
 VERSION AL558928.3 GI:46184315  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 977)  
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization.  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:31283061.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 2801.r  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?e=CS0DJ007AE04QPI&c=2801.r.  
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FEATURES  
 source

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 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 66.5%; Score 762; DB 1; Length 977;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 812; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 70 TGGAGCTGTCCGGCTCGCCCGCCCGCTTCTGTGCTATGCTCTGGCTGACATTCGGGG 129  
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 QY 86 CGCGTGTGTACGCGTGGACCGCCCGCTCCCGCTACGACGTGAGCCGCTTGGCCCGGG 145  
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 QY 130 CGCGTGTGTACGCGTGGACCGCCCGCTCCCGCTACGACGTGAGCCGCTTGGCCCGGG 189  
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 QY 190 GCAAGCCTCGCTAGTCTGACCTGAAGCAGCCCGCGGAGCCCGCTGCTGCGGGCTC 249  
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 QY 250 TGTCAAGCGCTCGATGTCTGCTGAGCCCTTCCCGCGGCTCATGAGAGAACTCC 309  
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RESULT 5  
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 LOCUS BQ962523

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DEFINITION  AGENCOURT_8817570 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6379327
5', mRNA sequence.
ACCESSION   BQ962523
VERSION     BQ962523.1 GI:22378001
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 890)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LCM2566 row: c column: 08
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                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."
ORIGIN
Query Match 57.9%; Score 664; DB 5; Length 890;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 714; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 128 CCGCTGTGTAGCTGGACCGCGCGCGCTCCCGCTACGACGTGAGCGCTTGGCGCGG 187
QY 146 GCAAGCGCTCGCTAGTGTGGACCTTGAAGCAGCGCGCGCGCGCTGCTGGCGGTC 205
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QY 206 TGTGCAAGCGGTCCGATGTGCTGTGGAGCCCTTCGCGCGCGGTGTCTGGAAGAACTCC 265
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DB 428 TGTCCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC 487
QY 446 TCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGTGCACCTGGGCAATTATATGCTCTTTT 505
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DB 668 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACACAGATGGGG 727
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DB 728 AATTCATGCTGTGGAGCAATAGAACCCAGTCTTACGAGCTGCTGATCAAGG 782

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DEFINITION 602631843P1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776971 5',
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ACCESSION   BG741165
VERSION     BG741165.1 GI:14051818
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 955)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LAM10630 row: f column: 12
            High quality sequence stop: 805.
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                Average insert size 1.5kb. Library constructed by Life
                Technologies. Note: this is a NCI CGAP Library."
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 785; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 GCGCTCGTACTGCTGGACCTGAGCAGCCCGGGAGCCCGCTGCTGCGGCTGTG 60

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 VERSION AL545355.3 GI:45745838  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1081)  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:31267191.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with NotI and cloned  
 into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 2801.r

For more information about this cluster, see  
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 digested with NotI and cloned into the NotI and EcoRV  
 sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 52.4%; Score 601; DB 1; Length 1081;  
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 Qy 421 GAGATCCGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGGT 480  
 Db 430 GAGATCCGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGGT 489  
 Qy 481 GCATGGGCAATTAATATGGCTTTTGGCCAGTCAGGAAGCTTCTGACGCGGGAATCCA 540  
 Db 490 GCATGGGCAATTAATATGGCTTTTGGCCAGTCAGGAAGCTTCTGACGCGGGAATCCA 549  
 Qy 541 GATGCAATATGTTGGAGGAAGCAAGCATATTTAAGTCTTTTCTGTGTGGAAACTCAGAAA 600  
 Db 550 GATGCAATATGTTGGAGGAAGCAAGCATATTTAAGTCTTTTCTGTGTGGAAACTCAGAAA 609  
 Qy 601 T 601  
 Db 610 T 610

RESULT 8

B0638373  
LOCUS B0638373 649 bp mRNA linear EST 15-JUL-2002  
DEFINITION hd21903.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
Homo sapiens cDNA clone hd21903 5', mRNA sequence.  
ACCESSION B0638373  
VERSION B0638373.1 GI:21762832  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 649)  
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
TITLE Expressed sequence tag analysis of human retina for the NEIBank  
Project: Retbindin, an abundant, novel retinal cDNA and alternative  
splicing of other retina-preferred gene transcripts  
Mol. Vis. 8 (4), 196-204 (2002)  
JOURNAL 22103461  
MEDLINE 12107411  
PubMed Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 21 row: g column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1..649  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="hd21903"  
/tissue\_type="Retina"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retina cDNA (Un-normalized,  
unamplified): hd/he"  
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
the protocols of the SuperScript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTAGTCTCAGATCGAGCGCGCC(T)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."  
ORIGIN  
Query Match 51.4%; Score 589; DB 5; Length 649;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 150 GCGCTCGTGTAGTGTGGACCTGAAGCAGCGCGGGAGCGCGGTGTGCGCGGTGTGTG 209  
DB 10 GCGCTCGTGTAGTGTGGACCTGAAGCAGCGCGGGAGCGCGGTGTGCGCGGTGTGTG 69  
QY 210 CAAGCGGTGGATGTGCTGTGGAGCCCTTCGCGCGGTGTGTCATGGAGAACTCCAGCT 269  
DB 70 CAAGCGGTGGATGTGCTGTGGAGCCCTTCGCGCGGTGTGTCATGGAGAACTCCAGCT 129  
QY 270 GGGCCACAGATCTTGCACCGGGAAATCCAGAGCTTATTTATGCGAGCTGAGTGGATT 329  
DB 130 GGGCCACAGATCTTGCACCGGGAAATCCAGAGCTTATTTATGCGAGCTGAGTGGATT 189  
QY 330 TGGCCAGTCAGGAAGCTTCTGCGCGGTAGTGTGGCCACGATATCAACTATTGGCTTTGTC 389

Db 190 TGGCCAGTCAGGAAGCTTCTGCCGTTAGTGGCCACGATATCAACTATTGGCTTTGTC 249  
QY 390 AGGTGTTCTTCAAAAATTTGGCAGAGTGGTGAAGATCCGATATCCCGCTGAATCTCCT 449  
Db 250 AGGTGTTCTTCAAAAATTTGGCAGAGTGGTGAAGATCCGATATCCCGCTGAATCTCCT 309  
QY 450 GGCTGACTTTGCTGCTGGTGGCTTATGTGTGCTGGCATTATATGGCTCTTTTGA 509  
Db 310 GGCTGACTTTGCTGCTGGTGGCTTATGTGTGCTGGCATTATATGGCTCTTTTGA 369  
QY 510 CCGCACACGACTGGCAAGGTCAGGTCAATGATGCAAAATATGTTGGGAAGCAACAGCATA 569  
Db 370 CCGCACACGACTGACAAAGGTCAGGTCAATGATGCAAAATATGTTGGGAAGCAACAGCATA 429  
QY 570 TTTAAGTCTTTCTGTGGAAAACTCAAGAAATCGAGTCTGTGGGAAGCACTTCGAGGACA 629  
Db 430 TTTAAGTCTTTCTGTGGAAAACTCAAGAAATCGAGTCTGTGGGAAGCACTTCGAGGACA 489  
QY 630 GAACATGTTGGATGCTGGAGCACCCTTTCTATACACTTACAGGACAGATGGGAATT 689  
Db 490 GAACATGTTGGATGCTGGAGCACCCTTTCTATACACTTACAGGACAGATGGGAATT 549  
QY 690 CATGCTGTTGGAGCAATAGAAACCCAGTCTTACGAGCTGCTGATCAAGGACTTGGACT 749  
Db 550 CATGCTGTTGGAGCAATAGAAACCCAGTCTTACGAGCTGCTGATCAAGGACTTGGACT 609  
QY 750 AAGTCTGATGAACCTTCCCAATCAGATCAGATGATGAT 789  
Db 610 AAGTCTGATGAACCTTCCCAATCAGATGATGATGAT 649  
RESULT 9  
BI256255 602975075F1 NIH\_MGC\_12 Homo sapiens cDNA clone IMAGE:5114130 5',  
LOCUS mRNA sequence.  
ACCESSION BI256255  
VERSION BI256255.1 GI:14810488  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 808)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbe-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1277 row: f column: 19  
High quality sequence stop: 751.  
Location/Qualifiers  
1..808  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5114130"  
/tissue\_type="cervical carcinoma cell line"  
/lab\_host="DH10B"  
/clone\_lib="NIH MGC 12"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.4 kb. Library prepared by Life  
Technologies."  
ORIGIN

Query Match 49.9%; Score 572; DB 4; Length 808;  
Best Local Similarity 100.0%; Pred. No. 1.3e-307; Indels 0; Gaps 0;  
Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

28 GAGCTGTCCGGCTGGCCCGCCGCGCTTCTGTCTATGTCCTGGCTGACTTCGGGGCG 87  
1 GAGCTGTCCGGCTGGCCCGCCGCGCTTCTGTCTATGTCCTGGCTGACTTCGGGGCG 60  
88 CGTGTGTACGGTGGACCGGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGGGC 147  
61 CGTGTGTACGGTGGACCGGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGGGC 120  
148 AAGCGCTCGTAGTCTGACCTGAAGCAGCGCGGGGAGCGCGCTGCTGCGGCTG 207  
121 AAGCGCTCGTAGTCTGACCTGAAGCAGCGCGGGGAGCGCGCTGCTGCGGCTG 180  
208 TCGAAGCGGTGGATGTCTGTGAGCGCTTCCGCGCGGTGTGATGAGAACTCCAG 267  
181 TCGAAGCGGTGGATGTCTGTGAGCGCTTCCGCGCGGTGTGATGAGAACTCCAG 240  
268 CTGGCCCGCAGAGATTCTGAGCGGGAATAATCAAGGCTTATTTATGCGAGCTGAGTGA 327  
241 CTGGCCCGCAGAGATTCTGAGCGGGAATAATCAAGGCTTATTTATGCGAGCTGAGTGA 300  
328 TTTGGCCAGTCAGGAGCTTCTGCGGTTAGTGGCCACGATATCAACTATTGGCTTTG 387  
301 TTTGGCCAGTCAGGAGCTTCTGCGGTTAGTGGCCACGATATCAACTATTGGCTTTG 360  
388 TCAGGTGTTCTCAAAAATTGGCAGAGTGTGAGAAATCCGTTATGCCCGCTGAATCTC 447  
361 TCAGGTGTTCTCAAAAATTGGCAGAGTGTGAGAAATCCGTTATGCCCGCTGAATCTC 420  
448 CTGGCTGACTTGTGTGGTGGCTTATGTGTGACATGGGCAATTAATGGCTCTTTT 507  
421 CTGGCTGACTTGTGTGGTGGCTTATGTGTGACATGGGCAATTAATGGCTCTTTT 480  
508 GACCCACACGACCTGCAAGGTCAGGTCAATGATGCAATATGTCGGAAGGACAGCA 567  
481 GACCCACACGACCTGCAAGGTCAGGTCAATGATGCAATATGTCGGAAGGACAGCA 540  
568 TATTTAAGTCTTTTCTGTGGAATACTCAGAA 599  
541 TATTTAAGTCTTTTCTGTGGAATACTCAGAA 572

RESULT 10  
AL558977  
LOCUS AL558977 893 bp mRNA linear EST 02-APR-2004  
DEFINITION AL558977 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED  
ACCESSION AL558977  
VERSION AL558977.3 GI:46184364  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 893)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31283110.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
2801.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DJ008AF04QP1&c=2801.r.

FEATURES  
source Location/Qualifiers  
1..893  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DJ008VK07"  
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/cell\_line="JURKAT"  
/clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
/notes="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 49.9%; Score 572; DB 1; Length 893;  
Best Local Similarity 99.7%; Pred. No. 1.3e-307; Indels 0; Gaps 0;  
Matches 672; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 26 TGGAGCTGTCCGGCTGGCCCGCCGCGTTCGTCTGTCTATGTCCTGGCTGACTTCGGGG 85  
Db 115 TGGAGCTGTCCGGCTGGCCCGCCGCGTTCGTCTGTCTATGTCCTGGCTGACTTCGGGG 174  
Qy 86 CGCGTGTGGTACGGTGGACCGGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 145  
Db 175 CGCGTGTGGTACGGTGGACCGGCGCGCTCCCGCTACGACGTGAGCGCTTGGGCGGG 234  
Qy 146 GCAAGCGCTCGCTAGTGTCTGGAACCTGAAGCAGCGCGGGAGCGCGCTGTCTGGCGGTC 205  
Db 235 GCAAGCGCTCGCTAGTGTCTGGAACCTGAAGCAGCGCGGGAGCGCGCTGTCTGGCGGTC 294  
Qy 206 TGTGCAAGCGGTGGATGTCTGTCTGAGCGCTTCCCGCGCGTGTCTATGAGAACTCC 265  
Db 295 TGTGCAAGCGGTGGATGTCTGTCTGAGCGCTTCCCGCGCGTGTCTATGAGAACTCC 354  
Qy 266 AGCTGGGCGCCAGAGATTCTGCAGCGGGAATAATCAAGGCTTATTTATGCCAGGCTGAGTG 325  
Db 355 AGCTGGGCGCCAGAGATTCTGCAGCGGGAATAATCAAGGCTTATTTATGCCAGGCTGAGTG 414  
Qy 326 GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 385  
Db 415 GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 474  
Qy 386 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGTGAGAAATCCGATATGCCCGCTGAATC 445  
Db 475 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGTGAGAAATCCGATATGCCCGCTGAATC 534  
Qy 446 TCCTGGCTGACTTGTCTGGTGGTGGCTTATGTGTGCACTGGGCAATTAATATGCTCTTT 505  
Db 535 TCCTGGCTGACTTGTCTGGTGGTGGCTTATGTGTGCACTGGGCAATTAATATGCTCTTT 594  
Qy 506 TTGACCCGACACGACCTGGCAAGGCTCAGGTCATTTGATGCAAAATATGGTGGAAAGAACAG 565  
Db 595 TTGACCCGACACGACCTGACAGAGGTCAGGTCATTTGATGCAAAATATGGTGGAAAGAACAG 654  
Qy 566 CATATTTAAGTCTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACTCGAG 625  
Db 655 CATATTTAAGTCTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACTCGAG 714  
Qy 626 GACAGACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGACATGGGG 685  
Db 715 GACAGACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGACATGGGG 774  
Qy 686 AATTCATGGCTGTT 699  
Db 775 AATTCATGGCTGTT 788

RESULT 11  
CN305057

LOCUS CN305057 622 bp mRNA linear EST 16-MAY-2004  
DEFINITION 17000424183299 GRN\_ES Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN305057  
VERSION CN305057.1 GI:47321471  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 622)  
Li, Y., Xu, C., Fang, R., Guebler, K., Rao, M.S., Mandalam, R.,  
Lebrowski, J. and Stanton, J.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 622 Std Error: 0.00.  
Location/Qualifiers  
1..622  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, cell lines H1, H7, and H9"  
/clone\_lib="GRN ES"  
/note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"  
FEATURES  
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1..622  
Query Match 49.6%; Score 568; DB 7; Length 622;  
Best Local Similarity 99.8%; Pred. No. 2.2e-305;  
Matches 618; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 149 AGCGCTCGTAGTGTGGACCTGGAAGCAGCCGGGGAGCCCGCTGCGCGCTGT 208  
DB 4 AGCGCTCGTAGTGTGGACCTGGAAGCAGCCGGGGAGCCCGCTGCGCGCTGT 63  
QY 209 GCAAGCGGTGCGATGCTGCTGGAGCCCTTCGCGCGGTGTCTATGGAGAACTCCAGC 268  
DB 64 GCAAGCGGTGCGATGCTGCTGGAGCCCTTCGCGCGGTGTCTATGGAGAACTCCAGC 123  
QY 269 TGGGCCCCAGAGATTCTGACGCGGGAATCCAAAGGCTTATTATGCCAGGCTGAGTGGAT 328  
DB 124 TGGGCCCCAGAGATTCTGACGCGGGAATCCAAAGGCTTATTATGCCAGGCTGAGTGGAT 183  
QY 329 TTGGCCAGTCAGGAAGCTTTCGCGGTAGCTGGCCACCATATCAACTATTTGGCTTTGT 388  
DB 184 TTGGCCAGTCAGGAAGCTTTCGCGGTAGCTGGCCACCATATCAACTATTTGGCTTTGT 243  
QY 389 CAGGTGTTCTCAAAAATTTGGCAGAAGTGTGAGAAATCCGTATGCCCGCTGAATCTCC 448  
DB 244 CAGGTGTTCTCAAAAATTTGGCAGAAGTGTGAGAAATCCGTATGCCCGCTGAATCTCC 303  
QY 449 TGGCTGACTTTGCTGTTGGCTTTATGTGTGCACTGGGCAATTAATATGGCTCTTTTGG 508  
DB 304 TGGCTGACTTTGCTGTTGGCTTTATGTGTGCACTGGGCAATTAATATGGCTCTTTTGG 363  
QY 509 ACCGCAACAGCATCTGCAAGGTCAGGTCAATTGATGCAAAATATGTTGGGAAGAACAGCAT 568  
DB 364 ACCGCAACAGCATCTGCAAGGTCAGGTCAATTGATGCAAAATATGTTGGGAAGAACAGCAT 423  
QY 569 ATTATGTTCTTTCTGTGGAACCTCAGAAATCGAGTCTGTGGGAAGCACTCCAGGAC 628  
DB 424 ATTATGTTCTTTCTGTGGAACCTCAGAAATCGAGTCTGTGGGAAGCACTCCAGGAC 483

QY 629 AGAATCATGTTGGATGTTGGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGAAT 688  
DB 484 AGAATCATGTTGGATGTTGGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGAAT 543  
QY 689 TCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGAGACTTGGAC 748  
DB 544 TCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGAGACTTGGAC 603  
QY 749 TAAAGTCTGATGAATCTCC 767  
DB 604 TAAAGTCTGATGAATCTCC 622  
RESULT 12  
BQ941482 890 bp mRNA linear EST 21-AUG-2002  
LOCUS BQ941482  
DEFINITION AGENCOURT 8821476 Lupski\_sciatic\_nerve Homo sapiens cDNA clone  
IMAGE:6203684 5', mRNA sequence.  
ACCESSION BQ941482  
VERSION BQ941482.1 GI:22356960  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 890)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM13623 row: 1 column: 21  
High quality sequence stop: 621.  
Location/Qualifiers  
1..890  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6203684"  
/sex="male"  
/tissue\_type="sciatic nerve"  
/dev\_stage="adult, 70 yr"  
/lab\_host="DH10B"  
/clone\_lib="Lupski\_sciatic\_nerve"  
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NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCACGCTCCG-3' and  
5'-GACTAGTTCTAGATCGAGCGGCGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.87 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."  
ORIGIN  
Query Match 49.5%; Score 567; DB 5; Length 890;  
Best Local Similarity 99.8%; Pred. No. 8.3e-305;  
Matches 617; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 396 TCTCTCAAAAATTTGCAGAAAGTGGTGAATCCCGTATCCCGCTGAATCTCTGGCTGA 455  
DB 1 TCTCTCAAAAATTTGCAGAAAGTGGTGAATCCCGTATCCCGCTGAATCTCTGGCTGA 60  
QY 456 CTTTGGCTGTTGGCTTTATGTGTGCACTGGGCAATTAATATGGCTCTTTTGGCGCAC 515



Db 61 CTTTCTGCTGGTGGCCTTATGTGTGCATCGGCATTATAATGGCTCTTTTGGCCGAC 120

Qy 516 AGCACTGCGAGGGTCAGGTCAATGATGCAAAATATGTTGGAAGAACAGCATATTTAAG 575

Db 121 AGCACTGCGAGGGTCAGGTCAATGATGCAAAATATGTTGGAAGAACAGCATATTTAAG 180

Qy 576 TTCTTTTCTGTGGAACCTCAGAAATCGAGTCTGTGGAAGCACCTCGAGGACAGAAAT 635

Db 181 TTCTTTTCTGTGGAACCTCAGAAATCGAGTCTGTGGAAGCACCTCGAGGACAGAAAT 240

Qy 636 GTTGATGTTGAGACACCTTTCTATACGACTTACAGGACAGGATGGGAAATCATGGC 695

Db 241 GTTGATGTTGAGACACCTTTCTATACGACTTACAGGACAGGATGGGAAATCATGGC 300

Qy 696 TGTTGAGCAATAGAACCCAGTCTTACGAGTCTGTATCAAGGACTTGGACTTAAAGTC 755

Db 301 TGTTGAGCAATAGAACCCAGTCTTACGAGTCTGTATCAAGGACTTGGACTTAAAGTC 360

Qy 756 TGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAAGAAAGTTTGC 815

Db 361 TGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAAGAAAGTTTGC 420

Qy 816 AGATGATTTGCAAGAGAGAGAGGAGAGAGTGTCAAAATCTTTTGACGACAGATGC 875

Db 421 AGATGATTTGCAAGAGAGAGAGGAGAGAGTGTCAAAATCTTTTGACGACAGATGC 480

Qy 876 CTGTGTGACTCGGTCTGACTTTTGGAGGAGTGTTCATCATGATCAACACAGGACG 935

Db 481 CTGTGTGACTCGGTCTGACTTTTGGAGGAGTGTTCATCATGATCAACACAGGACG 540

Qy 936 GGGCTCGTTTATCACAGTGGAGGAGCAGCATGTGAGCCCGCCCGCCCTGCTGCTGT 995

Db 541 GGGCTCGTTTATCACAGTGGAGGAGCAGCATGTGAGCCCGCCCGCCCTGCTGCTGT 600

Qy 996 AAACACCCGACCATCCC 1013

Db 601 AAACACCCGACCATCCC 618

RESULT 13

LOCUS CN305056 613 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000531862255 GRN\_ES Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN305056

VERSION CN305056.1 GI:47321470

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 613)

Li.Y., Xu.C., Fang.R., Guegler,K., Rao.M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.

TITLE Transcription characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 613 Std Error: 0.00.  
Location/Qualifiers  
1. .613  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/clone\_lib="GRN\_ES"

/note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 49.0%; Score 562; DB 7; Length 613;  
Best Local Similarity 99.8%; Pred. No. 5.1e-302;  
Matches 612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 GAGCTGTCCGGCTGGCCCGCCCGGCTTCTGTGCTATGTCCTGGCTGACTTGGGGCG 87

Db 1 GAGCTGTCCGGCTGGCCCGCCCGGCTTCTGTGCTATGTCCTGGCTGACTTGGGGCG 60

Qy 88 CGTGTGTGTAGCGTGGACCGCCCGCTCCCGCTACGACGTCGACCGCTTGGCCCGGGGC 147

Db 61 CGTGTGTGTAGCGTGGACCGCCCGCTCCCGCTACGACGTCGACCGCTTGGCCCGGGGC 120

Qy 148 AAGCGCTCGCTAGTGTGGACCTGAAGCAGCCGGGGAGCCCGCTGCTGCGCGCTGTG 207

Db 121 AAGCGCTCGCTAGTGTGGACCTGAAGCAGCCGGGGAGCCCGCTGCTGCGCGCTGTG 180

Qy 208 TGAAGCGGTGCGATGTGCTGTGAGCCCTTCCCGCGCGTGTCTATGAGAACTCCAG 267

Db 181 TGAAGCGGTGCGATGTGCTGTGAGCCCTTCCCGCGCGTGTCTATGAGAACTCCAG 240

Qy 268 CTGGGCCAGAGATTTCTGACGCGGAAATCCAAAGGCTTATTTATGCCAGCTCAGTGA 327

Db 241 CTGGGCCAGAGATTTCTGACGCGGAAATCCAAAGGCTTATTTATGCCAGCTCAGTGA 300

Qy 328 TTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTTTG 387

Db 301 TTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTTTG 360

Qy 388 TCAGGTGTTCTCAAAAATTTGGCAGAGTGGTGAAGATCCGTATGCCCGCTGAATCTC 447

Db 361 TCAGGTGTTCTCAAAAATTTGGCAGAGTGGTGAAGATCCGTATGCCCGCTGAATCTC 420

Qy 448 CTGGCTGACTTTGCTGGTGGCTTATGTGTCACCTGGGCATTATAATGGCTCTTTTT 507

Db 421 CTGGCTGACTTTGCTGGTGGCTTATGTGTCACCTGGGCATTATAATGGCTCTTTTT 480

Qy 508 GACCGCACGCACTGCAAGGGTCAGGTCAATGATCAAAATATGTTGGAAGGAAACAGCA 567

Db 481 GACCGCACGCACTGCAAGGGTCAGGTCAATGATCAAAATATGTTGGAAGGAAACAGCA 540

Qy 568 TATTTAAGTCTTTTCTGTGGAAGAACTCAGAAATCGAGTCTGTGGGAGCACTCGAGGA 627

Db 541 TATTTAAGTCTTTTCTGTGGAAGAACTCAGAAATCGAGTCTGTGGGAGCACTCGAGGA 600

Qy 628 CAGAACATGTTGG 640

Db 601 CAGAACATGTTGG 613

RESULT 14

LOCUS BG035606 812 bp mRNA linear EST 24-JAN-2001

DEFINITION 602325670F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4413833 5', mRNA sequence.

ACCESSION BG035606

VERSION BG035606.1 GI:12429907

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 812)

NH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC





Qy 541 GATGCAATATG 552  
|||||  
Db 572 GATGCAATATG 583

Search completed: July 27, 2005, 08:08:50  
Job time : 4262 secs